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<110> Pompejus, Markus .  
      Kroger, Burkhard  
      Schroder, Hartwig  
      Zelder, Oskar  
      Haberhauer, Gregor  
<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
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Glu Met Ala Arg Leu Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile
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Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu
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Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu
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375 380 385

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Thr Arg Gly Val Asp Val Gly Ala Lys Val Glu Ile Tyr Asn Ile Ile
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Asn Glu Met Thr Glu Lys Gly Gly Ala Val Leu Met Val Ser Ser Glu
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 Ile Thr His Asn Pro His His Ala Tyr Leu Val Gly Asp His Phe Ile
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185 190 195	
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Ser Leu Ala Gly Gly Thr Gly Lys Ala Thr Gly Thr Leu Ile Gly Ala
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Phe Val Ile Val Thr Ala Gly Ile Asp Leu Ser Val Gly Ser Val Ala
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Ala Leu Gly Ala Met Thr Ser Ala Tyr Phe Phe Ala Glu Val Gly Leu
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Pro Gly Trp Ile Thr Leu Leu Ile Gly Leu Phe Ile Gly Leu Leu Ala
 85 90 95

Gly Ala Ile Ser Gly Ile Ser Ile Ala Tyr Gly Lys Leu Pro Ala Phe
 100 105 110

Ile Ala Thr Leu Ala Met Met Ser Ile Ala Arg Gly Ile Thr Leu Val
 115 120 125

Ile Ser Gln Gly Ser Pro Ile Pro Ser Ala Pro Ala Val Asn Ala Leu
 130 135 140

Gly Arg Thr Tyr Phe Gly Ile Pro Met Pro Ile Leu Met Met Ala Leu
 145 150 155 160

Ala Gly Ile Val Cys Trp Phe Ile Leu Ser Arg Thr Val Leu Gly Arg
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Ser Met Tyr Ala Ile Gly Gly Asn Met Glu Ala Ala Arg Leu Ser Gly
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Leu Pro Val Lys Lys Ile Leu Val Met Val Tyr Ala Leu Ala Gly Val

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Met Ile Gly Ala Phe																	
1 5																	
gag ttc gga ttg ttg tac gga gtt gtc gca ttg ggc gtc tat ttg acg																	163
Glu Phe Gly Leu Leu Tyr Gly Val Val Ala Leu Gly Val Tyr Leu Thr																	
10 15 20																	
ttc cgt gtg ctc aac ttt ccc gac ctc acc gtt gac ggc agc ctg acc																	211
Phe Arg Val Leu Asn Phe Pro Asp Leu Thr Val Asp Gly Ser Leu Thr																	
25 30 35																	
act ggc gcg gca aca gct gcg aca gct ctt atg tct ggc tgg cct ccc																	259
Thr Gly Ala Ala Thr Ala Ala Thr Ala Leu Met Ser Gly Trp Pro Pro																	
40 45 50																	
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Leu Met Ala Thr Ala Ala Gly Phe Val Thr Gly Phe Ile Ala Gly Met																	
55 60 65																	
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Ile Thr Gly Leu Leu His Thr Lys Gly Lys Ile Asp Gly Leu Leu Ala																	
70 75 80 85																	

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 Gly Ile Leu Thr Met Ile Ala Leu Trp Ser Val Asn Leu Arg Ile Met
 90 95 100

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 Gly Gly Ala Asn Val Pro Leu Leu Arg Thr Asp Asn Leu Phe Thr Pro
 105 110 115

ctt cgc gac gcc ggc ctc ctc ggc aca tgg gca ggc ccg gcg atc ctc 499
 Leu Arg Asp Ala Gly Leu Leu Gly Thr Trp Ala Gly Pro Ala Ile Leu
 120 125 130

gcc gtt gca gtg gga att ttg gga ctc atc gtc atc tgg ttc ctc aac 547
 Ala Val Ala Val Gly Ile Leu Gly Leu Ile Val Ile Trp Phe Leu Asn
 135 140 145

act gat atc gga ctg tgc ctg cga tcc acc ggc gac aac ggg ccg atg 595
 Thr Asp Ile Gly Leu Ser Leu Arg Ser Thr Gly Asp Asn Gly Pro Met
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 170 175 180

tcc ctg tcc aat ggt ttt gtt ggt ctt gcc ggt gca ctc atc gct cag 691
 Ser Leu Ser Asn Gly Phe Val Gly Leu Ala Gly Ala Leu Ile Ala Gln
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tac cag ggc ttc gca gat att tgc atg ggt att ggc ctc atc gtg atc 739
 Tyr Gln Gly Phe Ala Asp Ile Ser Met Gly Ile Gly Leu Ile Val Ile
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 Gly Leu Ala Ser Val Ile Leu Gly Gln Ala Ile Phe Gly Gln Arg Arg
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 Val Trp Leu Ala Val Leu Ala Val Ile Val Gly Ala Ile Ala Tyr Arg
 230 235 240 245

ctg atc att ttc gca gca ctg cgc gtt ggc ctt gac ccc aac gat atg 883
 Leu Ile Ile Phe Ala Ala Leu Arg Val Gly Leu Asp Pro Asn Asp Met
 250 255 260

aag gca att tct gcg atc ttg gtg gtt gtc gcc atg ctg ctg ccg agg 931
 Lys Ala Ile Ser Ala Ile Leu Val Val Val Ala Met Leu Leu Pro Arg
 265 270 275

tgg cgt gcg aag ttc tcc aag gca ccg aag cct aag caa cca gta gca 979
 Trp Arg Ala Lys Phe Ser Lys Ala Pro Lys Pro Lys Gln Pro Val Ala
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<211> 296

<212> PRT

<213> Corynebacterium glutamicum

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Asp	Gly	Ser	Leu	Thr	Thr	Gly	Ala	Ala	Thr	Ala	Ala	Thr	Ala	Leu	Met
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Ser	Gly	Trp	Pro	Pro	Leu	Met	Ala	Thr	Ala	Ala	Gly	Phe	Val	Thr	Gly
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Phe	Ile	Ala	Gly	Met	Ile	Thr	Gly	Leu	Leu	His	Thr	Lys	Gly	Lys	Ile
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Asp	Gly	Leu	Leu	Ala	Gly	Ile	Leu	Thr	Met	Ile	Ala	Leu	Trp	Ser	Val
				85					90					95	
Asn	Leu	Arg	Ile	Met	Gly	Gly	Ala	Asn	Val	Pro	Leu	Leu	Arg	Thr	Asp
			100					105					110		
Asn	Leu	Phe	Thr	Pro	Leu	Arg	Asp	Ala	Gly	Leu	Leu	Gly	Thr	Trp	Ala
		115					120					125			
Gly	Pro	Ala	Ile	Leu	Ala	Val	Ala	Val	Gly	Ile	Leu	Gly	Leu	Ile	Val
	130					135						140			
Ile	Trp	Phe	Leu	Asn	Thr	Asp	Ile	Gly	Leu	Ser	Leu	Arg	Ser	Thr	Gly
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Asp	Asn	Gly	Pro	Met	Val	Gln	Ser	Phe	Gly	Val	Ser	Thr	Asp	Phe	Thr
				165					170					175	
Lys	Ile	Leu	Thr	Ile	Ser	Leu	Ser	Asn	Gly	Phe	Val	Gly	Leu	Ala	Gly
			180					185					190		
Ala	Leu	Ile	Ala	Gln	Tyr	Gln	Gly	Phe	Ala	Asp	Ile	Ser	Met	Gly	Ile
		195					200					205			
Gly	Leu	Ile	Val	Ile	Gly	Leu	Ala	Ser	Val	Ile	Leu	Gly	Gln	Ala	Ile
	210					215						220			
Phe	Gly	Gln	Arg	Arg	Val	Trp	Leu	Ala	Val	Leu	Ala	Val	Ile	Val	Gly
225					230					235					240
Ala	Ile	Ala	Tyr	Arg	Leu	Ile	Ile	Phe	Ala	Ala	Leu	Arg	Val	Gly	Leu
				245					250					255	
Asp	Pro	Asn	Asp	Met	Lys	Ala	Ile	Ser	Ala	Ile	Leu	Val	Val	Val	Ala
			260					265					270		
Met	Leu	Leu	Pro	Arg	Trp	Arg	Ala	Lys	Phe	Ser	Lys	Ala	Pro	Lys	Pro
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<223> RXA02439
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Ser Gly Glu Ala Ser Thr Ser Ile Val Glu Arg Ala Leu Lys Arg Pro

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gaa ctg acc agc ctg ctt ggc gcc gtg ctt gtt ttt acg ctg ttt atg 211
Glu Leu Thr Ser Leu Leu Gly Ala Val Leu Val Phe Thr Leu Phe Met
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gtg gtc gcg ccg gca ttt agg tca tgg gat tcg atg gcg acc gtg ctg 259
Val Val Ala Pro Ala Phe Arg Ser Trp Asp Ser Met Ala Thr Val Leu
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Tyr	Ala	Ser	Ser	Thr	Ile	Gly	Ile	Met	Ala	Val	Ala	Val	Gly	Leu	Leu	
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Met Ile Ala Asp Glu Phe Asp Leu Ser Thr Gly Val Ala Val Thr Thr
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gca gcg ctg gcg gcc tcg atg ttt agc tat aac ctg tgg ctg aac acc 403
Ala Ala Leu Ala Ala Ser Met Phe Ser Tyr Asn Leu Trp Leu Asn Thr
90 95 100

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Trp	Val	Gly	Ala	Leu	Ile	Ala	Leu	Val	Ile	Ser	Leu	Ala	Ile	Gly	Phe	
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Thr Leu Ala Thr Phe Leu Met Leu Gln Gly Ile Asn Leu Ala Val Thr
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aag ctg att tcc ggc acc gtg gcc acg cca acc atc gcg gat atg gaa 595
Lys Leu Ile Ser Gly Thr Val Ala Thr Pro Thr Ile Ala Asp Met Glu
150 155 160 165

ggt ttt cct tca gcg cgt gcg gtg ttt gcc agc tcg att ccc atc ttt 643
Gly Phe Pro Ser Ala Arg Ala Val Phe Ala Ser Ser Ile Pro Ile Phe
170 175 180

ggt gtg aat att cgc atc act gtt ttt tgg tgg ctg ctg ttt gtt atc 691

Gly Val Asn Ile Arg Ile Thr Val Phe Trp Trp Leu Leu Phe Val Ile
 185 190 195

gtc ggc act ttt gtg ttg ttt aag acg cgc atc ggc aac tgg att ttt 739
 Val Gly Thr Phe Val Leu Phe Lys Thr Arg Ile Gly Asn Trp Ile Phe
 200 205 210

gcg gtc ggt ggc gat gaa gag gca gct cgc gca gtc ggc gtt ccc gtg 787
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 215 220 225

cgt ggc gtg aaa atc ggc ctg ttc atg ttc gtt ggt ttt gcc gcc tgg 835
 Arg Gly Val Lys Ile Gly Leu Phe Met Phe Val Gly Phe Ala Ala Trp
 230 235 240 245

ttt gtg ggc atg cac aac ctg ttc ctc ttt gat tgc att cag gct ggt 883
 Phe Val Gly Met His Asn Leu Phe Leu Phe Asp Ser Ile Gln Ala Gly
 250 255 260

caa ggc gtg ggt aat gag ttc ctc tac atc atc gct gcg gtg atc gga 931
 Gln Gly Val Gly Asn Glu Phe Leu Tyr Ile Ile Ala Ala Val Ile Gly
 265 270 275

ggc atc tcc atg act ggt ggc cgc gga aca gtg gtg ggc aca atg att 979
 Gly Ile Ser Met Thr Gly Gly Arg Gly Thr Val Val Gly Thr Met Ile
 280 285 290

ggt gca ctc atc ttt gga atg acc aac caa ggc att gtt tat gca ggt 1027
 Gly Ala Leu Ile Phe Gly Met Thr Asn Gln Gly Ile Val Tyr Ala Gly
 295 300 305

tgg aac cct gac tgg ttc atg ttc ttc ctc ggc ggc acc cta ctt ctg 1075
 Trp Asn Pro Asp Trp Phe Met Phe Phe Leu Gly Gly Thr Leu Leu Leu
 310 315 320 325

gct gtt ttg ctc aat cac cga ttc gag cgt ttc aac aag gag cga tca 1123
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tgacagacct cattcaactc cgc 1146

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 <213> Corynebacterium glutamicum

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 35 40 45

Met Ala Thr Val Leu Tyr Ala Ser Ser Thr Ile Gly Ile Met Ala Val
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<223> RXN02994

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Thr Asp Ile Asp Leu Glu Ile Pro Arg Gly Gln Val Val Val Val Leu	
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Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg	
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ctc gaa acc atc gag gaa ggc acc atc gaa atc gat gga aag gtt ctc	192
Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Val Leu	
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cca gaa gaa ggt aaa ggc tta gcc aat ctc cgc gcc gat gtc gga atg	240
Pro Glu Glu Gly Lys Gly Leu Ala Asn Leu Arg Ala Asp Val Gly Met	
65 70 75 80	
gta ttc cag tcc ttc aac ctc ttc ccc cac ctc acc atc aaa gac aac	288
Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn	
85 90 95	
gtc act ctt gca ccc atc aaa gtg cga aag atg aaa aag tct gaa gcc	336
Val Thr Leu Ala Pro Ile Lys Val Arg Lys Met Lys Lys Ser Glu Ala	
100 105 110	
gaa aag ctt gcg atg agc ctg ttg gaa cgc gtc ggc atc gca aac caa	384
Glu Lys Leu Ala Met Ser Leu Leu Glu Arg Val Gly Ile Ala Asn Gln	
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gct gat aaa tat ccg gcg caa ctg tcc ggc ggt cag caa cag cgt gtg	432
Ala Asp Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Arg Val	
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Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp	
145 150 155 160	
gag ccc acc tcc gcc ctt gac cct gaa atg gtc aac gaa gtg ttg gac	528
Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp	
165 170 175	
gtc atg gca agc ctt gcc aag gaa ggc atg acg atg gtg tgt gtt acc	576
Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val Thr	
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cac gag atg gga ttc gca cgc aaa gca gcc gat cgt gtg ttg ttc atg	624
His Glu Met Gly Phe Ala Arg Lys Ala Ala Asp Arg Val Leu Phe Met	
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Ala Asp Gly Leu Ile Val Glu Asp Thr Glu Pro Asp Ser Phe Phe Thr	
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 <223> FRXA01245

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Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His Trp	
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ctg gag atg cgc gct ctt ggt gca gcc tcc tcc gcg ctt gac gcg ctg	144
Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala Leu	
35 40 45	
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Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr Thr	
50 55 60	
cgc acc gta gcg atc tca gag ctg gcc gtc gac gat gtc gtg ctg gtc	240
Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu Val	
65 70 75 80	
cga gca ggt gcc cgc gtc ccg gcc gac ggg acc atc atg gac gga gcg	288
Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Met Asp Gly Ala	
85 90 95	
gcc gaa ttc gat gag gcc atg atc acc ggc gaa tcc cga ccc gtc tac	336
Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val Tyr	
100 105 110	
cgg gat acc ggt gag acc gtg gtg gcc ggc acc gtg gcc acc gac aac	384
Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp Asn	
115 120 125	
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Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu Ala	
130 135 140	
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Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg Ala	
145 150 155 160	
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Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala Leu	
165 170 175	
atc acg gcc ctg atc acc gcc gtg gtc tgg acc atc atc ggc agc ccc	576
Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser Pro	
180 185 190	

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cac atg cgc acc atc gac gtc gtc ttg ttc gat aag acc ggc acc ctg His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr Leu 245 250 255	768
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gcc gac atc acc ggt tcc tgg gca cag cga ggt gcc gga gtg cta cat Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu His 355 360 365	1104
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 gcc gag gtc ggt att gcg att ggc gcg ggt aca gat gtg gcg atg gag 1440
 Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met Glu
 465 470 475 480
 tcc gcc ggg gtg gtc ctg gcc agt gat gat ccc ccg gcc gtg ctg tcg 1488
 Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu Ser
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 Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala Gly
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 gtg ctg gcc cct atc ggt gtg ctg ctt ccc ccg gcg gcg gcc gcc atc 1632
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 530 535 540
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 Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu Leu
 545 550 555 560
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 Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly Lys
 565 570 575
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 35 40 45
 Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr Thr
 50 55 60
 Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu Val

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Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Met Asp Gly Ala	85	90	95
Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val Tyr	100	105	110
Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp Asn	115	120	125
Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu Ala	130	135	140
Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg Ala	145	150	155
Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala Leu	165	170	175
Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser Pro	180	185	190
Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys Pro	195	200	205
His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser Glu	210	215	220
Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu Glu	225	230	235
His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr Leu	245	250	255
Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly Ile	260	265	270
Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Ala Glu Ala Asp Ser	275	280	285
Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala Ala His Pro	290	295	300
Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala Ser	305	310	315
Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val Gly	325	330	335
Gly Pro Asn Met Leu Arg Glu Phe Asn Leu Thr Thr Pro Gly Glu Leu	340	345	350
Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu His	355	360	365
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Category	Sub-category	Value
1. General Information	1.1. Name of the Project	Project X
	1.2. Date of Submission	2023-10-27
	1.3. Author's Name	John Doe
	1.4. Institution	ABC University
	1.5. Supervisor's Name	Dr. Jane Smith
	1.6. Title of the Thesis	Exploring the Impact of AI on Modern Education
	1.7. Degree Program	Master of Science in Education
	1.8. Field of Study	Education Technology
	1.9. Advisor's Email	john.doe@abc.edu
	1.10. Contact Information	+91 98765 43210
2. Abstract	2.1. Summary of the Study	This study explores the impact of Artificial Intelligence (AI) on modern education, focusing on personalized learning and data-driven decision-making.
	2.2. Objectives	The primary objective is to analyze the effectiveness of AI-based learning management systems (LMS) in improving student outcomes.
	2.3. Methodology	The research employs a quantitative approach, utilizing surveys and data analysis to measure the impact of AI on student performance.
	2.4. Results	The findings indicate a significant positive correlation between the use of AI-based LMS and improved student engagement and learning outcomes.
	2.5. Conclusion	The study concludes that AI-based LMS has the potential to revolutionize education by providing personalized learning experiences.
	2.6. Keywords	Artificial Intelligence, Education Technology, Learning Management Systems, Student Outcomes.
	2.7. Introduction	The rapid advancement of AI technology has opened new avenues for educational innovation, particularly in the realm of personalized learning.
	2.8. Literature Review	Previous research has shown that AI-based LMS can adapt to individual student needs, leading to higher retention rates and better understanding of complex topics.
	2.9. Significance of the Study	This study contributes to the existing body of knowledge by providing empirical evidence on the effectiveness of AI-based LMS in a real-world educational context.
	2.10. Future Research	Further research is needed to explore the long-term effects of AI-based LMS on student learning and to identify potential challenges and limitations.

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Leu Val Thr Leu Lys Thr Pro Gly Leu Val Thr Pro Ala Pro Val Asp		
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Ile Asp Glu Ala Ala Ser Lys Val Ser Val Ile Pro Val Asp Ala Ala		
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Gln Ala Pro Thr Ala Tyr Gln Glu Gly Arg Pro Ala Ile Ile Asn Asn		
195	200	205
Ser Phe Leu Asp Arg Ala Gly Ile Asp Pro Asn Leu Ala Val Phe Glu		
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Asp Asp Pro Glu Ser Glu Glu Ala Glu Pro Tyr Ile Asn Val Phe Val		
225	230	235 240
Thr Lys Ala Glu Asp Lys Asp Asp Ala Asn Ile Ala Arg Leu Val Glu		
245	250	255
Leu Trp His Asp Pro Glu Val Leu Ala Ala Val Asp Arg Asp Ser Glu		
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Met Arg Ile Ser Ser															5
1															
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Lys Leu Val Thr Thr Ala Leu Leu Ala Ala Ile Ser Leu Phe Gly Ile															20
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Ser Thr Ala Gln Ala Gln Asp Ile Phe Asp Gly Gly Arg Leu Ala Gly															35
25 30															
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Gly Ser Ser Gln Val Ser Asn Leu Ser Ser Val Pro Glu Asn Leu Ala															50
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Leu Pro Glu Ile Glu Asn Ser Ile Asp Leu Glu Arg Tyr Lys Gly Lys															65
55 60															
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Trp Tyr Gln Val Ala Ala Ile Pro Gln Pro Phe Ser Leu Gln Cys Ser															85
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His Asp Val Thr Ala Asp Tyr Gly Val Ile Asp Ser Asp Thr Ile Ser															100
90 95															
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Val Thr Asn Lys Cys Gly Thr Phe Phe Gly Pro Ser Val Ile Glu Gly															115
105 110															
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Ser Ala Lys Val Val Ser Asn Ala Ser Leu Lys Val Ser Phe Pro Gly															130
120 125															
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Ile Pro Phe Gln Ser Glu Asp Asn Gln Ala Asn Tyr Arg Val Thr Tyr															145
135 140															
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Ile Glu Asp Asp Tyr Ser Leu Ala Ile Val Gly Ser Pro Ser Arg Ser															165
150 155 160															
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Ser Gly Phe Ile Leu Ser Arg Thr Pro Gln Leu Ser Ser Asp Gln Trp															180
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Ser His Val Arg Asn Ile Thr Glu Asp Ser Gly Trp Trp Pro Cys Ala															195
185 190															
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Phe Ile Thr Val Pro Ala Thr Gly Gly Leu Asn Thr Ala Thr Pro Leu															210
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Cys Thr Leu															

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Pro Glu Asn Leu Ala Leu Pro Glu Ile Glu Asn Ser Ile Asp Leu Glu
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Arg Tyr Lys Gly Lys Trp Tyr Gln Val Ala Ala Ile Pro Gln Pro Phe
 65 70 75 80

Ser Leu Gln Cys Ser His Asp Val Thr Ala Asp Tyr Gly Val Ile Asp
 85 90 95

Ser Asp Thr Ile Ser Val Thr Asn Lys Cys Gly Thr Phe Phe Gly Pro
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Ser Val Ile Glu Gly Ser Ala Lys Val Val Ser Asn Ala Ser Leu Lys
 115 120 125

Val Ser Phe Pro Gly Ile Pro Phe Gln Ser Glu Asp Asn Gln Ala Asn
 130 135 140

Tyr Arg Val Thr Tyr Ile Glu Asp Asp Tyr Ser Leu Ala Ile Val Gly
 145 150 155 160

Ser Pro Ser Arg Ser Ser Gly Phe Ile Leu Ser Arg Thr Pro Gln Leu
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Ser Ser Asp Gln Trp Ser His Val Arg Asn Ile Thr Glu Asp Ser Gly
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 Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn
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Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg
40 45 50

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Thr Val Val Gln Gly Met Leu Leu Gly Phe Val His Gly Leu Val Thr
70 75 80 85

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Tyr	Val	Ala	Leu	Ser	Val	Val	Glu	Ala	Leu	Tyr	Ser	Ile	Ala	Leu	Gly	
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Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu Arg Ser Ser Trp Pro
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ccg ttg gct aat ctc gca gcg ctt ggt ggg gta gcg ttt gtc act ttt 643
Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val Ala Phe Val Thr Phe
170 175 180

aag cga ctg gcc ggc gca atc atc acc gcg agt gtg att gct atc ggc 739
Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser Val Ile Ala Ile Gly
200 205 210

gcg gtg tca tcc ctg tac gtt gac cgc aat ggc acg agc gat gaa agc 787

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Phe	Asn	Ala	Gln	Arg	Arg	Ala	Val	Leu	Ala	Asn	His	Ala	Arg	Glu	Thr		
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ctc	aag	ctg	gat	gaa	caa	gtg	gat	ttg	gtg	atc	tgg	ccg	gag	aat	tcc	931	
Leu	Lys	Leu	Asp	Glu	Gln	Val	Asp	Leu	Val	Ile	Trp	Pro	Glu	Asn	Ser		
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Ser	Asp	Val	Asn	Pro	Phe	Ser	Asp	Ala	Gln	Ala	Arg	Ala	Ile	Ile	Asp		
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Val	Asp	Glu	Val	Gly	Pro	Arg	Asn	Thr	Met	Gln	Val	Phe	Asp	Pro	Val		
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Glu	Gly	Ala	Ala	Glu	Tyr	His	Asn	Lys	Lys	Phe	Leu	Gln	Pro	Phe	Gly		
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gaa	tac	atg	ccg	ttt	cgc	gaa	ttc	ctg	aga	att	ttc	tcg	ccc	tac	gtt	1171	
Glu	Tyr	Met	Pro	Phe	Arg	Glu	Phe	Leu	Arg	Ile	Phe	Ser	Pro	Tyr	Val		
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Asp	Ser	Ala	Gly	Asn	Phe	Gln	Pro	Gly	Asp	Gly	Thr	Gly	Val	Val	Glu		
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	375				380						385						
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Cys	Tyr	Glu	Val	Ile	Phe	Asp	Arg	Ala	Gly	Arg	Asp	Ala	Ile	Ala	Asn		
390				395						400					405		
ggg	gct	gaa	ttt	ttg	acc	acg	ccc	acc	aac	aac	gcc	acc	ttc	gga	ttc	1363	
Gly	Ala	Glu	Phe	Leu	Thr	Thr	Pro	Thr	Asn	Asn	Ala	Thr	Phe	Gly	Phe		
				410					415					420			
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Thr	Asp	Met	Thr	Tyr	Gln	Gln	Leu	Ala	Met	Ser	Arg	Met	Arg	Ala	Ile		
			425				430						435				
gaa	ttt	gat	agg	gcg	gtg	gtt	gtt	gca	gct	aca	tcg	ggc	gtt	tcg	gct	1459	
Glu	Phe	Asp	Arg	Ala	Val	Val	Val	Ala	Ala	Thr	Ser	Gly	Val	Ser	Ala		
		440				445						450					
atc	gtc	aac	cct	gat	gga	agc	att	tcc	caa	aac	acc	cga	att	ttt	gag	1507	
Ile	Val	Asn	Pro	Asp	Gly	Ser	Ile	Ser	Gln	Asn	Thr	Arg	Ile	Phe	Glu		

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Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu Val Ile Ile Gly			
	490	495	500
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Ala Lys Gly Ser Ala Arg Pro Ala Gln Val Arg Val Lys Lys Val Pro			
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Gly Thr Ala Leu Phe Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val			
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Pro Gln Lys Arg Arg Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln			
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Met Ser Thr Gly Pro Thr Val Val Gln Gly Met Leu Leu Gly Phe Val			
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His Gly Leu Val Thr Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe			
	85	90	95
Val Gly Ser Leu Pro Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr			
	100	105	110
Ser Ile Ala Leu Gly Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp			
	115	120	125
Trp Lys Val Leu Leu Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu			
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Arg Ser Ser Trp Pro Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp			
145	150	155	160

Gly Gln Ile Asn Gly Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val
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 Ala Phe Val Thr Phe Ser Thr Val Leu Ala Ala Val Gly Val Ala Met
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 Val Ile Ile Ser Lys Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser
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 Val Ile Ala Ile Gly Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly
 210 215 220
 Thr Ser Asp Glu Ser Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro
 225 230 235 240
 Arg Met Gly Leu Asp Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn
 245 250 255
 His Ala Arg Glu Thr Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile
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 Trp Pro Glu Asn Ser Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala
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 Arg Ala Ile Ile Asp Gly Ala Val Glu His Val Gln Ala Pro Ile Leu
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 Val Gly Thr Ile Thr Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln
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 Val Phe Asp Pro Val Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe
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 Leu Gln Pro Phe Gly Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile
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 Phe Ser Pro Tyr Val Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly
 355 360 365
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 Val Gly Val Met Thr Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg
 385 390 395 400
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 405 410 415
 Ala Thr Phe Gly Phe Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser
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 Arg Met Arg Ala Ile Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr
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 Ser Gly Val Ser Ala Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn
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Val Thr Leu Phe Val 5																
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Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn 20																
gaa ccg atc ggc tgg ttt gtc gcg gga att gtt ggc act gca tta ttt 211																
Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val Gly Thr Ala Leu Phe 35																
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Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg 50																
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Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln Met Ser Thr Gly Pro 65																
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Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg Asp Ala Ile Ala Asn			
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Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn Ala Thr Phe Gly Phe			
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Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn Thr Arg Ile Phe Glu			
	455	460	465
gcc gcc acc ttg acg gaa tcc att cca ctc aag gac act gtc acc atc			1555
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Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn Ser Arg Ser Lys Ser			
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 Pro Gln Lys Arg Arg Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln
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Met Ser Ser Glu Ala
1 5

gta gat gct acg acg ctg gtg att att cca acg tac aac gag ctg gaa 163
Val Asp Ala Thr Thr Leu Val Ile Ile Pro Thr Tyr Asn Glu Leu Glu
10 15 20

aac ctt cca ctc atc gtg gat cgc gtg cgc acc gca acc cct gag gtt 211
Asn Leu Pro Leu Ile Val Asp Arg Val Arg Thr Ala Thr Pro Asp Val
25 30 35

cac gta ctc atc gtg gac gac aac agc cca gac ggc acc ggc gag cgc 259
His Val Leu Ile Val Asp Asp Asn Ser Pro Asp Gly Thr Gly Glu Arg
40 45 50

gca gac aag ctt gct gct gac gac gac cac att ttt gtc ctc cac cgc 307
Ala Asp Lys Leu Ala Ala Asp Asp Asp His Ile Phe Val Leu His Arg
55 60 65

gaa ggc aaa ggc ggc ctg tgc gca gag tac atg gct ggc ttc cag tgg 355

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Glu Gly Lys Gly Gly Leu Cys Ala Glu Tyr Met Ala Gly Phe Gln Trp
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 Gly Leu Glu Arg Asp Tyr Gln Val Leu Cys Glu Met Asp Ala Asp Gly
 90 95 100
 tcc cac gca cca gaa cag ctg cac ctg ctg ctc gct gag atc acc aat 451
 Ser His Ala Pro Glu Gln Leu His Leu Leu Leu Ala Glu Ile Thr Asn
 105 110 115
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 Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro Gly Gly Arg Val
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 gtc aac tgg ccc aag aac cgt tgg ctc ttg tcc aag ggc ggc aac gtc 547
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 135 140 145
 tac atc agc gtc gcg ctc ggc gcc ggc ttg acc gat atg acc gca ggc 595
 Tyr Ile Ser Val Ala Leu Gly Ala Gly Leu Thr Asp Met Thr Ala Gly
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 Tyr Arg Ala Phe Arg Arg Glu Val Leu Glu Ala Leu Pro Leu Asp Glu
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Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser Pro Asp	35	40	45
Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp His Ile	50	55	60
Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu Tyr Met	65	70	75
Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu Cys Glu	85	90	95
Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu Leu Leu	100	105	110
Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val	115	120	125
Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu Leu Ser	130	135	140
Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly Leu Thr	145	150	155
Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu Glu Ala	165	170	175
Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Glu	180	185	190
Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu Val Pro	195	200	205
Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp Gly Ser	210	215	220
Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu Lys His	225	230	235
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Pro Asp Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp	
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His Ile Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu	
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Tyr Met Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu	
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Cys Glu Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu	
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ctg ctc gct gag atc acc aat ggc gct gac ctg gtc atc ggc tcg cgc	288
Leu Leu Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg	
85 90 95	
tac gtg cca ggc ggc cgc gta gtc aac tgg ccc aag aac cgt tgg ctc	336
Tyr Val Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu	
100 105 110	
ttg tcc aag ggc ggc aac gtc tac atc agc gtc gcg ctc ggc gcc ggc	384
Leu Ser Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly	
115 120 125	
ttg acc gat atg acc gca ggc tac cgc gct ttt cga cgt gaa gtg cta	432
Leu Thr Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu	
130 135 140	
gaa gca ctg ccg ctt gat gag ctc tcc aac gct ggc tac att ttc caa	480
Glu Ala Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln	
145 150 155 160	
gtt gag att gcc tac cgt gca gtt gaa gcc gga ttc gat gtt cgt gaa	528
Val Glu Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu	
165 170 175	
gtt ccc atc act ttc acc gag cgt gag atc ggc gaa tcc aag ctg gac	576
Val Pro Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp	
180 185 190	
ggc agc ttt gtc aag gat tcc ctg ctc gag gta acc aag tgg ggc ctc	624
Gly Ser Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu	
195 200 205	
aag cac cgc ggt ggc cag gcc aag gaa ctg tcc aag gaa atg gtc ggc	672
Lys His Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly	
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ctg ctg aac tat gag tgg aag cac ttc aaa aag cgc aac acc tgg ctc	720
Leu Leu Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu	
225 230 235 240	

G E G A T T A C C A G G C G G C A A C G T C T A C A T C A G C G T C T C G A A G T T C A A G L U A L A L E U P R O L E U A S P G L U L E U S E R A S N A L A G L Y T Y R I L E P H E G L N

743

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His	Ile	Phe	Val	Leu	His	Arg	Glu	Gly	Lys	Gly	Gly	Leu	Cys	Ala	Glu	
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Tyr	Met	Ala	Gly	Phe	Gln	Trp	Gly	Leu	Glu	Arg	Asp	Tyr	Gln	Val	Leu	
	50					55					60					
Cys	Glu	Met	Asp	Ala	Asp	Gly	Ser	His	Ala	Pro	Glu	Gln	Leu	His	Leu	
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Leu	Leu	Ala	Glu	Ile	Thr	Asn	Gly	Ala	Asp	Leu	Val	Ile	Gly	Ser	Arg	
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Tyr	Val	Pro	Gly	Gly	Arg	Val	Val	Asn	Trp	Pro	Lys	Asn	Arg	Trp	Leu	
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Leu	Ser	Lys	Gly	Gly	Asn	Val	Tyr	Ile	Ser	Val	Ala	Leu	Gly	Ala	Gly	
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	130					135					140					
Glu	Ala	Leu	Pro	Leu	Asp	Glu	Leu	Ser	Asn	Ala	Gly	Tyr	Ile	Phe	Gln	
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Val	Pro	Ile	Thr	Phe	Thr	Glu	Arg	Glu	Ile	Gly	Glu	Ser	Lys	Leu	Asp	
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Lys	His	Arg	Gly	Gly	Gln	Ala	Lys	Glu	Leu	Ser	Lys	Glu	Met	Val	Gly	
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 Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala Ala Ala Leu Phe Asp
 215 220 225

gag tcc gtg cag ctt gtg ctc tgt gcc ggc gcg cca gac acc ccc gaa 835
 Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala Pro Asp Thr Pro Glu
 230 235 240 245

atc gca gct cgc acc acc gcc ctg gtg gaa gaa ctc cag gca aag cgc 883
 Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Leu Gln Ala Lys Arg
 250 255 260

gaa ggc att ttc tgg gtt cag gac atg ctg ggc aag gac aaa atc caa 931
 Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly Lys Asp Lys Ile Gln
 265 270 275

gag att ctc acc gct gct gac acc ttc gtg tgc cca tcc att tac gag 979
 Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys Pro Ser Ile Tyr Glu
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 Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala Cys Asn Thr Ala Val
 295 300 305

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 330 335 340

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 360 365 370

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Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala	50	55	60
Ile Iys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn	65	70	75
Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His	85	90	95
Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser	100	105	110
Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr	115	120	125
Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala	130	135	140
Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr	145	150	155
Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp	165	170	175
Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser	180	185	190
Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe	195	200	205
Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala	210	215	220
Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala	225	230	235
Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu	245	250	255
Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly	260	265	270
Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys	275	280	285
Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala	290	295	300
Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val	305	310	315
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Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val 25 30 35																
cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc 259																
His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly 40 45 50																
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Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala Ile Lys Thr Leu Ser 55 60 65																
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Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn Val Asp Val Val His 70 75 80 85																
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His Gly Ile Pro His Val Ala Thr Ala His Ser Leu Glu Pro Asp Arg 105 110 115																
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Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr Asp Val Ser Ser Trp																

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	150					155					160					
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 <213> Corynebacterium glutamicum

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 Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala
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 Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn
 65 70 75 80
 Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His
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 Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser
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 Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr
 115 120 125
 Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala
 130 135 140
 Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr
 145 150 155 160
 Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp
 165 170 175
 Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser
 180 185 190
 Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe
 195 200 205
 Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala
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 Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala
 225 230 235 240

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Leu Gly Arg Pro Pro
1 5

cca gga gac gtt cat act ctc cta gac gat atc gga gca gag gaa tct 163
Pro Gly Asp Val His Thr Leu Leu Asp Asp Ile Gly Ala Glu Glu Ser
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gaa gca gat aaa gtt cca att gaa tgg caa aac gcc ctg act aag gca 211
Glu Ala Asp Lys Val Pro Ile Glu Trp Gln Asn Ala Leu Thr Lys Ala
25 30 35

gac agg tat gca aac cgg caa cac atg tct cag gca cga ctc tat cgc 259
Asp Arg Tyr Ala Asn Arg Gln His Met Ser Gln Ala Arg Leu Tyr Arg
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Val Ala Glu Ser Phe Leu Pro Asn Val Asn Gly Val Thr Asn Ser Val
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Ile Ala Pro Gly Ala Arg Asp Phe Glu Glu Glu Ile Gly His Tyr Leu
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Gly Ala Ala Ala Phe Ala Ala Arg Gln Leu Arg Ile Pro Ala Ile Ala
105 110 115

ccg ttg gcc act gca agc tgg gaa tgg atc aag acg gtc cac aac atg 547
Pro Leu Ala Thr Ala Ser Trp Glu Trp Ile Lys Thr Val His Asn Met
135 140 145

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Asp His Gly Ile Asn Asp Ile Phe His Trp Ala Arg Gly Val Asp Ser
170 175 180

gat cca agt gga gca aag aag atc gtt ggt ttc gtt ggg cgc ctt gca 739
Asp Pro Ser Gly Ala Lys Lys Ile Val Gly Phe Val Gly Arg Leu Ala
200 205 210

tcc gaa aag ggc gtg gag cgc ctt gct gga tta tcc gga cgc tca gac 787
Ser Glu Lys Gly Val Glu Arg Leu Ala Gly Leu Ser Gly Arg Ser Asp

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Glu Met Met Pro Asp Ala Ile Phe Thr Gly Ala Leu Gly Gly Glu Glu			
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Leu Ala Thr Thr Tyr Ala Ser Leu Asp Leu Phe Val His Pro Gly Glu			
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ttt gaa acc ttc tgc cag gcg atc cag gaa gcc caa gca tca ggt gtg			979
Phe Glu Thr Phe Cys Gln Ala Ile Gln Glu Ala Gln Ala Ser Gly Val			
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ccc acc att ggc cca cgc gca ggt ggt ccc att gat ttg atc aac gaa			1027
Pro Thr Ile Gly Pro Arg Ala Gly Gly Pro Ile Asp Leu Ile Asn Glu			
	295	300	305
ggc gtc aac ggc ctg ctt ctt gat gtt gta gat ttc aag gaa acc ctc			1075
Gly Val Asn Gly Leu Leu Leu Asp Val Val Asp Phe Lys Glu Thr Leu			
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Pro Ala Ala Ala Glu Trp Ile Leu Asp Asp Ser Arg His Ser Glu Met			
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Cys Ala Ala Ala Trp Glu Gly Val Lys Asp Lys Thr Trp Glu Ala Leu			
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tgc acc cag ctt ctc cag cac tac gcg gat gta atc gca ttg tca cag			1219
Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val Ile Ala Leu Ser Gln			
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cgc atc cca ctg aca ttc ttt ggc cct agc gct gaa gta gca aag ctt			1267
Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala Glu Val Ala Lys Leu			
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Val	Pro	Leu	Ile	Asp	Ser	Leu	Pro	Ile	Gly	Val	Pro	Leu	Pro	Ser	Val		
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Thr	Ser	Val	Leu	Arg	Glu	Tyr	Asn	Pro	Asp	Ile	Ile	His	Leu	Ala	Ser		
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Pro	Phe	Val	Leu	Gly	Gly	Ala	Ala	Ala	Phe	Ala	Ala	Arg	Gln	Leu	Arg		
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Ile	Pro	Ala	Ile	Ala	Ile	Tyr	Gln	Thr	Asp	Val	Ala	Gly	Phe	Ser	Gln		
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Arg	Tyr	His	Leu	Ala	Pro	Leu	Ala	Thr	Ala	Ser	Trp	Glu	Trp	Ile	Lys		
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Thr	Val	His	Asn	Met	Cys	Gln	Arg	Thr	Leu	Ala	Pro	Ser	Ser	Met	Ser		
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Ile	Asp	Glu	Leu	Arg	Asp	His	Gly	Ile	Asn	Asp	Ile	Phe	His	Trp	Ala		
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Arg	Gly	Val	Asp	Ser	Lys	Arg	Phe	His	Pro	Gly	Lys	Arg	Ser	Val	Ala		
			180					185					190				
Leu	Arg	Lys	Ser	Trp	Asp	Pro	Ser	Gly	Ala	Lys	Lys	Ile	Val	Gly	Phe		
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Val	Gly	Arg	Leu	Ala	Ser	Glu	Lys	Gly	Val	Glu	Arg	Leu	Ala	Gly	Leu		
210						215					220						
Ser	Gly	Arg	Ser	Asp	Ile	Gln	Leu	Val	Ile	Val	Gly	Asp	Gly	Pro	Glu		
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Ala	Lys	Tyr	Leu	Gln	Glu	Met	Met	Pro	Asp	Ala	Ile	Phe	Thr	Gly	Ala		
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Leu	Gly	Gly	Glu	Glu	Leu	Ala	Thr	Thr	Tyr	Ala	Ser	Leu	Asp	Leu	Phe		
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Gln	Ala	Ser	Gly	Val	Pro	Thr	Ile	Gly	Pro	Arg	Ala	Gly	Gly	Pro	Ile		
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Asp	Leu	Ile	Asn	Glu	Gly	Val	Asn	Gly	Leu	Leu	Leu	Asp	Val	Val	Asp		
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Phe	Lys	Glu	Thr	Leu	Pro	Ala	Ala	Ala	Glu	Trp	Ile	Leu	Asp	Asp	Ser		
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Thr Trp Glu Ala Leu Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val
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Ile Ala Leu Ser Gln Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala
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 Met Arg Val Ala Met
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 Gly Gly Met Asn Val Tyr Ile Leu Ser Thr Ala Thr Glu Leu Ala Lys
 25 30 35

cag ggt atc gag gtc gat att tac act cgt gcc acg agg cct tct cag 259
 Gln Gly Ile Glu Val Asp Ile Tyr Thr Arg Ala Thr Arg Pro Ser Gln
 40 45 50

ggt gag atc gtg aga gta gct gag aat ttg cgg gtc att aat atc gct 307
 Gly Glu Ile Val Arg Val Ala Glu Asn Leu Arg Val Ile Asn Ile Ala
 55 60 65

gcg ggg ccg tat gag ggg ctt tcc aaa gag gag ctt cct act cag ttg 355
 Ala Gly Pro Tyr Glu Gly Leu Ser Lys Glu Glu Leu Pro Thr Gln Leu
 70 75 80 85

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 Ala Ala Phe Thr Gly Gly Met Leu Ser Phe Thr Arg Arg Glu Lys Val
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 Thr Tyr Asp Leu Ile His Ser His Tyr Trp Leu Ser Gly Gln Val Gly
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 Trp Leu Leu Arg Asp Leu Trp Arg Ile Pro Leu Ile His Thr Ala His

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Glu	Ser	Glu	Ala	Arg	Arg	Ile	Cys	Glu	Gln	Gln	Leu	Val	Asp	Asn	Ala	
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gac	gtg	ttg	gcg	gtg	aac	act	cag	gag	gag	atg	cag	gat	ttg	atg	cat	643
Asp	Val	Leu	Ala	Val	Asn	Thr	Gln	Glu	Glu	Met	Gln	Asp	Leu	Met	His	
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cac	tac	gat	gcg	gat	ccg	gat	cgg	att	tct	gtg	gtg	tca	ccg	ggc	gcg	691
His	Tyr	Asp	Ala	Asp	Pro	Asp	Arg	Ile	Ser	Val	Val	Ser	Pro	Gly	Ala	
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Asp	Val	Glu	Leu	Tyr	Ser	Pro	Gly	Asn	Asp	Arg	Ala	Thr	Glu	Arg	Ser	
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Arg	Arg	Glu	Leu	Gly	Ile	Pro	Leu	His	Thr	Lys	Val	Val	Ala	Phe	Val	
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Gly	Arg	Leu	Gln	Pro	Phe	Lys	Gly	Pro	Gln	Val	Leu	Ile	Lys	Ala	Val	
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gcg	gcg	ttg	ttt	gat	cgc	gat	ccg	gac	cga	aat	ctg	cgc	gtc	att	att	883
Ala	Ala	Leu	Phe	Asp	Arg	Asp	Pro	Asp	Arg	Asn	Leu	Arg	Val	Ile	Ile	
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Cys	Gly	Gly	Pro	Ser	Gly	Pro	Asn	Ala	Thr	Pro	Asp	Thr	Tyr	Arg	His	
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Met	Ala	Glu	Glu	Leu	Gly	Val	Glu	Lys	Arg	Ile	Arg	Phe	Leu	Asp	Pro	
		280					285					290				
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Arg	Pro	Pro	Ser	Glu	Leu	Val	Ala	Val	Tyr	Arg	Ala	Ala	Asp	Ile	Val	
	295					300					305					
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Ala	Val	Pro	Ser	Phe	Asn	Glu	Ser	Phe	Gly	Leu	Val	Ala	Met	Glu	Ala	
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Gln	Ala	Ser	Gly	Thr	Pro	Val	Ile	Ala	Ala	Arg	Val	Gly	Gly	Leu	Pro	
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 Thr Arg Ile Arg Met Gly Glu Asp Ala Val Glu His Ala Arg Thr Phe
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 35 40 45

Thr Arg Pro Ser Gln Gly Glu Ile Val Arg Val Ala Glu Asn Leu Arg
 50 55 60

Val Ile Asn Ile Ala Ala Gly Pro Tyr Glu Gly Leu Ser Lys Glu Glu
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Leu Pro Thr Gln Leu Ala Ala Phe Thr Gly Gly Met Leu Ser Phe Thr
 85 90 95

Arg Arg Glu Lys Val Thr Tyr Asp Leu Ile His Ser His Tyr Trp Leu
 100 105 110

Ser Gly Gln Val Gly Trp Leu Leu Arg Asp Leu Trp Arg Ile Pro Leu
 115 120 125

Ile His Thr Ala His Thr Leu Ala Ala Val Lys Asn Ser Tyr Arg Asp
 130 135 140

Asp Ser Asp Thr Pro Glu Ser Glu Ala Arg Arg Ile Cys Glu Gln Gln
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Leu Val Asp Asn Ala Asp Val Leu Ala Val Asn Thr Gln Glu Glu Met
 165 170 175

Gln Asp Leu Met His His Tyr Asp Ala Asp Pro Asp Arg Ile Ser Val
 180 185 190

Val Ser Pro Gly Ala Asp Val Glu Leu Tyr Ser Pro Gly Asn Asp Arg
 195 200 205

445660-74660500

Ala Thr Glu Arg Ser Arg Arg Glu Leu Gly Ile Pro Leu His Thr Lys
 210 215 220

Val Val Ala Phe Val Gly Arg Leu Gln Pro Phe Lys Gly Pro Gln Val
 225 230 235 240

Leu Ile Lys Ala Val Ala Ala Leu Phe Asp Arg Asp Pro Asp Arg Asn
 245 250 255

Leu Arg Val Ile Ile Cys Gly Gly Pro Ser Gly Pro Asn Ala Thr Pro
 260 265 270

Asp Thr Tyr Arg His Met Ala Glu Leu Gly Val Glu Lys Arg Ile
 275 280 285

Arg Phe Leu Asp Pro Arg Pro Pro Ser Glu Leu Val Ala Val Tyr Arg
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Ala Ala Asp Ile Val Ala Val Pro Ser Phe Asn Glu Ser Phe Gly Leu
 305 310 315 320

Val Ala Met Glu Ala Gln Ala Ser Gly Thr Pro Val Ile Ala Ala Arg
 325 330 335

Val Gly Gly Leu Pro Ile Ala Val Ala Glu Gly Glu Thr Gly Leu Leu
 340 345 350

Val Asp Gly His Ser Pro His Ala Trp Ala Asp Ala Leu Ala Thr Leu
 355 360 365

Leu Asp Asp Asp Glu Thr Arg Ile Arg Met Gly Glu Asp Ala Val Glu
 370 375 380

His Ala Arg Thr Phe Ser Trp Ala Ala Thr Ala Ala Gln Leu Ser Ser
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Leu Tyr Asn Asp Ala Ile Ala Asn Glu Asn Val Asp Gly Glu Thr His
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His Gly

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 <223> RXN02595

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 Val Ile Val Val Ala
 1 5
 atg gct tcc att atg gct tgt tta aaa gca gct aga ctg aat aac cct 163

Variable	Mean	SD	Min	Max	Median	Q1	Q3	Mode	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.2	12.5	18	65	32	28	38	35	0.15	2.1	0.98	Normal
Gender	0.5	0.5	0	1	0.5	0.5	0.5	0.5	0.0	0.0	0.99	Normal
Marital Status	0.7	0.45	0	1	0.7	0.6	0.8	0.7	0.05	0.5	0.95	Normal
Education	12.5	2.5	9	16	12	11	13	12	0.1	1.5	0.99	Normal
Income	3000	1500	1000	6000	2500	2000	3500	3000	0.2	2.5	0.97	Normal
Occupation	1.5	1.0	1	3	1.5	1.5	2.0	1.5	0.0	0.0	0.99	Normal
Health Status	0.8	0.4	0	1	0.8	0.7	0.9	0.8	0.05	0.5	0.95	Normal
Stress Level	4.5	1.5	1	7	4.5	4.0	5.5	4.5	0.1	1.5	0.99	Normal
Life Satisfaction	5.5	1.0	3	7	5.5	5.0	6.0	5.5	0.0	0.0	0.99	Normal
Resilience	6.0	1.5	3	9	6.0	5.5	7.0	6.0	0.1	1.5	0.99	Normal
Optimism	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Emotional Stability	4.0	1.0	2	6	4.0	3.5	4.5	4.0	0.1	1.5	0.99	Normal
Self-Esteem	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Life Satisfaction	5.5	1.0	3	7	5.5	5.0	6.0	5.5	0.0	0.0	0.99	Normal
Resilience	6.0	1.5	3	9	6.0	5.5	7.0	6.0	0.1	1.5	0.99	Normal
Optimism	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Emotional Stability	4.0	1.0	2	6	4.0	3.5	4.5	4.0	0.1	1.5	0.99	Normal
Self-Esteem	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Life Satisfaction	5.5	1.0	3	7	5.5	5.0	6.0	5.5	0.0	0.0	0.99	Normal
Resilience	6.0	1.5	3	9	6.0	5.5	7.0	6.0	0.1	1.5	0.99	Normal
Optimism	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Emotional Stability	4.0	1.0	2	6	4.0	3.5	4.5	4.0	0.1	1.5	0.99	Normal
Self-Esteem	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Life Satisfaction	5.5	1.0	3	7	5.5	5.0	6.0	5.5	0.0	0.0	0.99	Normal
Resilience	6.0	1.5	3	9	6.0	5.5	7.0	6.0	0.1	1.5	0.99	Normal
Optimism	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Emotional Stability	4.0	1.0	2	6	4.0	3.5	4.5	4.0	0.1	1.5	0.99	Normal
Self-Esteem	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Life Satisfaction	5.5	1.0	3	7	5.5	5.0	6.0	5.5	0.0	0.0	0.99	Normal
Resilience	6.0	1.5	3	9	6.0	5.5	7.0	6.0	0.1	1.5	0.99	Normal
Optimism	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Emotional Stability	4.0	1.0	2	6	4.0	3.5	4.5	4.0	0.1	1.5	0.99	Normal
Self-Esteem	5.0	1.0	3	7	5.0	4.5	5.5	5.0	0.0	0.0	0.99	Normal
Life Satisfaction	5.5	1.0	3	7								

250 255 260

ctg ggt gtg agc gat cgc gtg gtt ttc cac ggc cag gtc gcc gag gat 931
 Leu Gly Val Ser Asp Arg Val Val Phe His Gly Gln Val Ala Glu Asp
 265 270 275

cac aag cac gcc ctg ttg gag cgc gcc acg att cat ctc atg cct tcg 979
 His Lys His Ala Leu Leu Glu Arg Ala Thr Ile His Leu Met Pro Ser
 280 285 290

cgc aag gaa ggc tgg ggc ctg gcg gtc acg gag gcg gcg cag cac ggc 1027
 Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu Ala Ala Gln His Gly
 295 300 305

gtt ccg acg atc ggt tac cga agc tca ggc ggc ctg cgc gat tcc gtc 1075
 Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly Leu Arg Asp Ser Val
 310 315 320 325

gtc gac ggc gaa acc ggc ctg ctt gtc gac tcc aag gcc gag ctt att 1123
 Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser Lys Ala Glu Leu Ile
 330 335 340

tca gcc acc aaa acc ctg ctt atc gac gcc tcc ctc cgc tcc aag ctc 1171
 Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser Leu Arg Ser Lys Leu
 345 350 355

ggc gcc agc gcg aag cag cgc gcc gaa aac tac aag tgg gac acc gcg 1219
 Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr Lys Trp Asp Thr Ala
 360 365 370

gga gcg cag ttc gag gaa cta ctt ctt ggt ctt gcg tcg aaa aag 1264
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 375 380 385

tagtcccagc ggcaacgccca tcc 1287

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 <212> PRT
 <213> Corynebacterium glutamicum

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Thr His Pro Gln Gly Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly
 35 40 45

Glu Phe Leu Ala Asp Gln Gly His Glu Val Val Phe Arg Thr Ala Gly
 50 55 60

His Thr Asp Ala Pro Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser
 65 70 75 80

Arg Ser Gly Gly Lys Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met
 85 90 95

Met Leu Gly Arg Val Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val
 100 105 110
 Val Asp Thr Gln Asn Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly
 115 120 125
 Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro
 130 135 140
 Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln
 145 150 155 160
 Ile Ala Pro Arg Ala Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu
 165 170 175
 Pro Ser Ala Glu Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile
 180 185 190
 His Ile Val Arg Asn Gly Val Asp Pro Val Pro Leu His Thr Pro Lys
 195 200 205
 Leu Asp Arg Asp Gly Gln His Ala Val Thr Leu Ser Arg Leu Val Pro
 210 215 220
 His Lys Gln Ile Glu His Ala Met Asp Val Val Ala Ala Leu Asp Gly
 225 230 235 240
 Val Val Leu Asp Val Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val
 245 250 255
 Asp Tyr Ala Arg Thr Leu Gly Val Ser Asp Arg Val Val Phe His Gly
 260 265 270
 Gln Val Ala Glu Asp His Lys His Ala Leu Leu Glu Arg Ala Thr Ile
 275 280 285
 His Leu Met Pro Ser Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu
 290 295 300
 Ala Ala Gln His Gly Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly
 305 310 315 320
 Leu Arg Asp Ser Val Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser
 325 330 335
 Lys Ala Glu Leu Ile Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser
 340 345 350
 Leu Arg Ser Lys Leu Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr
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 Ala Ser Lys Lys
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<213> Corynebacterium glutamicum

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<222> (101)..(751)

<223> FRXA02595

<400> 53

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                               Val Ile Val Val Ala
                               1 5

atg gct tcc att atg gct tgt tta aaa gca gct aga ctg aat aac cct 163
Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala Arg Leu Asn Asn Pro
                10                15                20

atg aag atc ctt ttg ttg tgc tgg cgt gat acc act cat cct caa ggt 211
Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr Thr His Pro Gln Gly
                25                30                35

ggc gga agt gaa cgc tat ctg gag cgg gtg ggt gag ttt ttg gcg gat 259
Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly Glu Phe Leu Ala Asp
                40                45                50

cag ggc cat gag gtg gtg ttt cgt act gct ggg cac acg gat gcg cca 307
Gln Gly His Glu Val Val Phe Arg Thr Ala Gly His Thr Asp Ala Pro
                55                60                65

cgg cgt tct ttc cgc gat ggt gtg agg tat tcc agg agc ggt ggg aag 355
Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser Arg Ser Gly Gly Lys
                70                75                80                85

ttt agt gtg tat ccc aag gcg tgg gtg gcc atg atg ttg ggt cgt gtg 403
Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met Met Leu Gly Arg Val
                90                95                100

ggg att ggc acg ttt tcc aag gtt gat gtg gtg gtg gat acg cag aat 451
Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val Val Asp Thr Gln Asn
                105                110                115

ggc att ccg ttt ttt gga aag ttt ttc tcc ggt aag ccg act gtg ttg 499
Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly Lys Pro Thr Val Leu
                120                125                130

ctc acg cat cat tgc cat aag gag cag tgg ccg gtg gtg ggt cgg gtg 547
Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val
                135                140                145

ctg gcg aag gtt ggt tgg ctg att gag agc cag atc gcg ccg cgc gct 595
Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln Ile Ala Pro Arg Ala
                150                155                160                165

tac aaa act gcg ccg tat gtg act gtt tca gag ccg agc gct gag gag 643
Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu
                170                175                180

ctc att gcg ttg ggt gtg gat cag cag cgg att cat atc gtg cgc aat 691
Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn
                185                190                195

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G G C C G G A A G G G A A A C C G G T C T T C T T T C G C G G C G C T G A G G A T G G T

cag cat gcg gtg 751
Gln His Ala Val
215

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Thr His Pro Gln Gly Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly
35 40 45

Glu Phe Leu Ala Asp Gln Gly His Glu Val Val Phe Arg Thr Ala Gly
50 55 60

His Thr Asp Ala Pro Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser
65 70 75 80

Arg Ser Gly Gly Lys Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met
85 90 95

Met Leu Gly Arg Val Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val
100 105 110

Val	Asp	Thr	Gln	Asn	Gly	Ile	Pro	Phe	Phe	Gly	Lys	Phe	Phe	Ser	Gly
		115					120					125			

Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro
130 135 140

Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln
145 150 155 160

Ile Ala Pro Arg Ala Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu
165 170 175

Pro Ser Ala Glu Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile
180 185 190

His Ile Val Arg Asn Gly Val Asp Pro Val Pro Leu His Thr Pro Lys
195 200 205

Leu Asp Arg Asp Gly Gln His Ala Val
210 215

$\langle 210 \rangle$	55
$\langle 211 \rangle$	834

185 190 195

atc gca ggc atg ggt agc cga gga ttc tcc acc ggc tcc cac ctc cac 739
 Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr Gly Ser His Leu His
 200 205 210

ttc gag gtt tac cct gca ggc ggt ggc gct gtt gat cca gct cct tgg 787
 Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val Asp Pro Ala Pro Trp
 215 220 225

ctt gca gag cgc ggc att act ctt taattaactt ttgggcgacc ctt 834
 Leu Ala Glu Arg Gly Ile Thr Leu
 230 235

<210> 56
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 56

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 20 25 30

Val Ser Thr Ala Gly Ala Gly Gly Ala Val Ala Ala Gln Ala Ser Asn
 35 40 45

Gln Pro Val Glu Val Asn Phe Glu Leu Thr Ala Asn Asp Thr Thr Asp
 50 55 60

Leu Val Ala Gly Ser Ser Ala Pro Gln Ile Leu Ser Ile Ala Glu Phe
 65 70 75 80

Lys Pro Val Val Asn Leu Gly Asp Gln Ile Val Lys Thr Ile Gln Tyr
 85 90 95

Asn Ala Asp Arg Ile Gln Ala Asp Leu Asp Ala Arg Gly Pro Ser Val
 100 105 110

Val Arg Pro Ala Glu Gly Ser Tyr Thr Ser Gly Phe Gly Ala Arg Trp
 115 120 125

Gly Thr Asn His Asn Gly Val Asp Ile Ala Asn Ala Ile Gly Thr Pro
 130 135 140

Ile Leu Ala Ala Met Asp Gly Thr Val Ile Asp Ala Gly Pro Ala Ser
 145 150 155 160

Gly Phe Gly Asn Trp Val Arg Leu Gln His Glu Asp Gly Thr Ile Thr
 165 170 175

Val Tyr Gly His Met Glu Thr Val Glu Val Thr Val Gly Gln Thr Val
 180 185 190

Lys Ala Gly Glu Arg Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr
 195 200 205

Gly Ser His Leu His Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val

210

215

220

Asp Pro Ala Pro Trp Leu Ala Glu Arg Gly Ile Thr Leu
 225 230 235

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 Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala
 20 25 30
 tca gat tgg ctc gca ttc ggt ggt gaa ggc gtg gga ccg tgg att gag 144
 Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
 35 40 45
 gat tct gcc tac gat gaa gcg cca gaa ata atc gga acc atg gaa ccg 192
 Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
 50 55 60
 gag tat gaa aag att gca gcg ctt gaa ccg gat ctg att ttg gac gtg 240
 Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
 65 70 75 80
 cgc agc tct ggc gac cag gaa cgc tat gac aag ttg tct tca atc gca 288
 Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
 85 90 95
 ctg acc atc ggc gtt cca gaa ggt ggc gat agc tac ctc acc cca cgc 336
 Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
 100 105 110
 gct gag cag gta acc atg atc gcc act gct ctg ggg cag gct gaa cgt 384
 Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
 115 120 125
 ggt gaa gaa gtg aac gct gaa tac gag cag ctc act gct gat att cgt 432
 Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg
 130 135 140
 gca gct cac ccg ggc tgg cct gag aag acc gcg gct gct gta tct gca 480
 Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala
 145 150 155 160
 acg gca acc agc tgg ggt gca tac atc aag ggc tcc aac cgt gta gat 528
 Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
 165 170 175

caq 866

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Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
          35          40          45
Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
          50          55          60
Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
          65          70          75          80
Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
          85          90          95
Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
          100          105          110
Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
          115          120          125

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Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly Asp Trp Phe Arg Phe
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 Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser Met Gly Gly Glu Asn
 70 75 80 85
 agc acc tgg atc ttt aca acc atc cag ttg agc ttc gtc atc ggt atc 403
 Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser Phe Val Ile Gly Ile
 90 95 100
 gca att tat gcc cca cgc atc aaa cac aag tgg atc gcg gca gga ctt 451
 Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp Ile Ala Ala Gly Leu
 105 110 115
 gcc ctt gtt gcc ggt gga gcc ttg gga aac gtg ttg gac cgg ttg ttc 499
 Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val Leu Asp Arg Leu Phe
 120 125 130
 aga gat cct tcc ttc ttc ttc gga cat gtt gtt gat tac atc tcc gta 547
 Arg Asp Pro Ser Phe Phe Phe Gly His Val Val Asp Tyr Ile Ser Val
 135 140 145
 gga aac ttt gca gta ttt aat atc gcc gat gcc tcg att tct tgc ggc 595
 Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala Ser Ile Ser Cys Gly
 150 155 160 165
 gtc gtg gtg ttc ctg atc gga atg ttc ctt gag gac cgt gaa aac gcc 643
 Val Val Val Phe Leu Ile Gly Met Phe Leu Glu Asp Arg Glu Asn Ala
 170 175 180
 cag cat gcc aaa gca act gac gag aag gat gag gcc tgatgaacaa 689
 Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu Ala
 185 190
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<210> 60
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 <213> Corynebacterium glutamicum

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 Ala Ala Ile Val Val Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln
 35 40 45
 Ile Met Leu Ser Trp Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly
 50 55 60
 Asp Trp Phe Arg Phe Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser
 65 70 75 80
 Met Gly Gly Glu Asn Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser
 85 90 95

BGI-131CP-1400000000

Phe Val Ile Gly Ile Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp
 100 105 110
 Ile Ala Ala Gly Leu Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val
 115 120 125
 Leu Asp Arg Leu Phe Arg Asp Pro Ser Phe Phe Phe Gly His Val Val
 130 135 140
 Asp Tyr Ile Ser Val Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala
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 Asp Arg Glu Asn Ala Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu
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Ala

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 <223> RXA01094

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 Met Thr Leu Ala Thr
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 Ile Pro Ser Pro Pro Gln Gly Val Trp Tyr Leu Gly Pro Ile Pro Ile
 10 15 20
 agg gcc tat gcg atg tgc atc atc gct ggc att att gtt gcc att tgg 211
 Arg Ala Tyr Ala Met Cys Ile Ile Ala Gly Ile Ile Val Ala Ile Trp
 25 30 35
 ctg acg aga aag cgc tac gcc gcc cgc ggt gga aac cct gaa atc gtc 259
 Leu Thr Arg Lys Arg Tyr Ala Ala Arg Gly Gly Asn Pro Glu Ile Val
 40 45 50
 ctt gat gca gcg atc gtg gca gtt cct gcc gga atc atc ggt gga cgc 307
 Leu Asp Ala Ala Ile Val Ala Val Pro Ala Gly Ile Ile Gly Gly Arg
 55 60 65
 att tat cac gtc att acc gac aac caa aag tac ttc tgc gat acc tgt 355
 Ile Tyr His Val Ile Thr Asp Asn Gln Lys Tyr Phe Cys Asp Thr Cys
 70 75 80 85
 aac ccc gtc gac gcc ttc aaa atc acc aac ggt ggt ctg gcc atc tgg 403

Asn Pro Val Asp Ala Phe Lys Ile Thr Asn Gly Gly Leu Gly Ile Trp
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 Gly Ala Val Ile Leu Gly Gly Leu Ala Val Ala Val Phe Phe Arg Tyr
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 aaa aag ctt cct ctt gca cct ttc gca gat gcc gtg gca cct gca gtt 499
 Lys Lys Leu Pro Leu Ala Pro Phe Ala Asp Ala Val Ala Pro Ala Val
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 atc ctg gcg cag gga att ggt cgt ctg ggc aac tgg ttt aac cag gag 547
 Ile Leu Ala Gln Gly Ile Gly Arg Leu Gly Asn Trp Phe Asn Gln Glu
 135 140 145
 ctc tac ggt gca gaa act acc gtt cca tgg gct ttg gaa atc tac tat 595
 Leu Tyr Gly Ala Glu Thr Thr Val Pro Trp Ala Leu Glu Ile Tyr Tyr
 150 155 160 165
 cgg gta gat gaa aat gga aaa ttc gca ccg gtg aca gga aca tcc acc 643
 Arg Val Asp Glu Asn Gly Lys Phe Ala Pro Val Thr Gly Thr Ser Thr
 170 175 180
 ggt gaa gta atg gct act gtt cat cca aca ttc ctc tat gaa ctg ttg 691
 Gly Glu Val Met Ala Thr Val His Pro Thr Phe Leu Tyr Glu Leu Leu
 185 190 195
 tgg aac cta ctg atc ttc gct ttg ttg atg tgg gct gac aag cga ttc 739
 Trp Asn Leu Leu Ile Phe Ala Leu Leu Met Trp Ala Asp Lys Arg Phe
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 Lys Leu Glu His Gly Arg Val Phe Ala Leu Tyr Val Ala Gly Tyr Thr
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 Leu Gly Arg Phe Trp Ile Glu Gln Met Arg Val Asp Glu Ala Thr Leu
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 gct tcg cca gat aga aaa ccc ttg ccg aaa gca ggg gag ggc att gat 1027
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gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat tct gaa gcc 979
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Asp Phe Val Val Arg Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly	50	55	60
Ser Val Ala Arg Leu Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg	65	70	75
Thr Phe Leu Arg Glu Gly Asn Phe Asp Val Leu His Ile His Glu Pro	85	90	95
Asn Ser Pro Ser Phe Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro	100	105	110
Ile Val Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys	115	120	125
Ala Phe Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly	130	135	140
Ile Ala Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly	145	150	155
Gly Asp Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys	165	170	175
Ala Ala Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu	180	185	190
Gly Arg Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala	195	200	205
Leu Thr Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly	210	215	220
Thr Pro Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp	225	230	235
Glu Glu Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro	245	250	255
Asn Thr Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala	260	265	270
Ala Gly Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val	275	280	285
Thr Asp Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly	290	295	300
Ser Asp Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro	305	310	315
Ser Ser Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala	325	330	335

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Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala	
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Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp	
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Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala	
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Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro	
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 Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg
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Variable	Mean	SD	Min	Max
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Marital status	0.6	0.5	0	1
Education	12.5	2.1	9	16
Income	15.2	8.5	5	35
Health status	0.7	0.4	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.4	0.5	0	1
Stress	0.6	0.5	0	1
Sleep	0.5	0.4	0	1
Appetite	0.6	0.5	0	1
Mood	0.5	0.4	0	1
Energy	0.6	0.5	0	1
Concentration	0.5	0.4	0	1
Memory	0.6	0.5	0	1
Emotion	0.5	0.4	0	1
Behavior	0.6	0.5	0	1
Thought	0.5	0.4	0	1
Feeling	0.6	0.5	0	1
Perception	0.5	0.4	0	1
Attention	0.6	0.5	0	1
Intuition	0.5	0.4	0	1
Imagination	0.6	0.5	0	1
Reasoning	0.5	0.4	0	1
Logic	0.6	0.5	0	1
Analysis	0.5	0.4	0	1
Synthesis	0.6	0.5	0	1
Evaluation	0.5	0.4	0	1
Comparison	0.6	0.5	0	1
Classification	0.5	0.4	0	1
Organization	0.6	0.5	0	1
Planning	0.5	0.4	0	1
Problem solving	0.6	0.5	0	1
Decision making	0.5	0.4	0	1
Communication	0.6	0.5	0	1
Interpersonal skills	0.5	0.4	0	1
Teamwork	0.6	0.5	0	1
Leadership	0.5	0.4	0	1
Management	0.6	0.5	0	1
Organization	0.5	0.4	0	1
Planning	0.6	0.5	0	1
Problem solving	0.5	0.4	0	1
Decision making	0.6	0.5	0	1
Communication	0.5	0.4	0	1
Interpersonal skills	0.6	0.5	0	1
Teamwork	0.5	0.4	0	1
Leadership	0.6	0.5	0	1
Management	0.5	0.4	0	1
Organization	0.6	0.5	0	1
Planning	0.5	0.4	0	1
Problem solving	0.6	0.5	0	1
Decision making	0.5	0.4	0	1
Communication	0.6	0.5	0	1
Interpersonal skills	0.5	0.4	0	1
Teamwork	0.6	0.5	0	1
Leadership	0.5	0.4	0	1
Management	0.6	0.5	0	1
Organization	0.5	0.4	0	1
Planning	0.6	0.5	0	1
Problem solving	0.5	0.4	0	1
Decision making	0.6	0.5	0	1
Communication	0.5	0.4	0	1
Interpersonal skills	0.6	0.5	0	1
Teamwork	0.5	0.4	0	1
Leadership	0.6	0.5	0	1
Management	0.5	0.4	0	1
Organization	0.6	0.5	0	1
Planning	0.5	0.4	0	1
Problem solving	0.6	0.5	0	1
Decision making	0.5	0.4	0	1
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cgt gca gct cag ggc gta gac cag gat tca ctt aag ggt tca ctg caa				883
Arg Ala Ala Gln Gly Val Asp Gln Asp Ser Leu Lys Gly Ser Leu Gln				
	250	255	260	
acc tac ttc gac gcg ctg tac gcc aac aat gac tcg cac cac gtt gcc				931
Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn Asp Ser His His Val Ala				
	265	270	275	
atg ttg gac ttc cgt aaa cag atc gaa gag ttc aac acc att ctc ggc				979
Met Leu Asp Phe Arg Lys Gln Ile Glu Glu Phe Asn Thr Ile Leu Gly				
	280	285	290	
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Ala Met Ser Leu Gly Ile Ser Ala Ile Gly Gly Ile Ser Leu Leu Val				
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ggt ggc atc gga gtg atg aac att atg ttg gtg tct gtc acc gag cga				1075
Gly Gly Ile Gly Val Met Asn Ile Met Leu Val Ser Val Thr Glu Arg				
	310	315	320	325
acc cgc gaa atc ggt gtc cga aaa gcc ctc ggc gct cgt cga cgt gac				1123
Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly Ala Arg Arg Arg Asp				
	330	335	340	
att cgc ctg caa ttc gtc gtt gaa gcc atg atc att tgt ttc atc ggt				1171
Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile Ile Cys Phe Ile Gly				
	345	350	355	
ggc atc ctc ggc gtg ctt ttg ggc ggc att ttg gga ttg atc atg toc				1219
Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu Gly Leu Ile Met Ser				
	360	365	370	
agc gct att ggc tac att tcc ttg cca cca ctg agt gga atc gtg atc				1267
Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu Ser Gly Ile Val Ile				
	375	380	385	
gcc ttg gta ttt tcc atg gct atc ggc ctg ttt ttc ggc tac tac ccc				1315
Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe Phe Gly Tyr Tyr Pro				
	390	395	400	405
gcc aac aag gca gca aag ctc gat cca att gac gcc ttg cgt tat gag				1363
Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp Ala Leu Arg Tyr Glu				
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1386

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Ala	Ser	Val	Ile	Gly	Ile	Leu	Thr	Ile	Gly	Lys	Ala	Leu	Gln	Asp	Gln
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Thr	Leu	Asn	Ser	Leu	Glu	Ser	Leu	Gly	Ala	Asn	Asp	Leu	Ser	Ala	Gln
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Val	Glu	Glu	Arg	Pro	Asp	Glu	Asp	Ser	Pro	Glu	Pro	Asp	Met	Phe	Ala
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Phe	Ser	Gly	Ala	Ala	Asn	Ser	Ser	Gly	Asn	Leu	Ile	Pro	Glu	Glu	Thr
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Val	Asp	Thr	Leu	Arg	Asp	Arg	Phe	Ala	Gly	Ser	Ile	Thr	Gly	Ile	Ser
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Val	Gly	Gly	Met	Gly	Thr	Gln	Gly	Thr	Leu	Ile	Gly	Asp	Thr	Ala	Asp
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Phe	Asp	Ala	Asn	Pro	Asn	Leu	Ala	Leu	Gly	Ser	Glu	Val	Ala	Phe	Glu
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Thr	Pro	Tyr	Thr	Val	Ala	Asn	Asp	Ile	Thr	His	Thr	Glu	Asp	Gly	Leu
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Asn	Thr	Leu	Ser	Ile	Arg	Ala	Ala	Gln	Gly	Val	Asp	Gln	Asp	Ser	Leu
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Lys	Gly	Ser	Leu	Gln	Thr	Tyr	Phe	Asp	Ala	Leu	Tyr	Ala	Asn	Asn	Asp
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 Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala Phe Ser Gly Ala Ala
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 aac tct agt ggc aat ctg att ccg gaa gaa aca gtt gat acg ctg cgc 403
 Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr Val Asp Thr Leu Arg
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 gat cgt ttc gca ggc agc atc acg gga atc agc gtt ggc gga atg ggt 451
 Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser Val Gly Gly Met Gly
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 acg caa ggc act ctc atc ggc gac acc gca gat ctt aaa tcc gat ctc 499
 Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp Leu Lys Ser Asp Leu
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 Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn Gly Val Glu Met Asn
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 Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala Ala Gln Arg Pro Val
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 gcg gtc atc gcc cca gac acc ttt aat acg ctt ttc gac gca aac ccc 643
 Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu Phe Asp Ala Asn Pro
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 aac ctc gct ctg ggg tcc gaa gta gct ttt gaa ctc aac ggt caa gag 691
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 185 190 195
 aca ttt ttg cgg gtt atc ggt gtg tat aaa gaa gcc gca gca ggt gga 739
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<213> Corynebacterium glutamicum

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 Ala Ser Val Ile Gly Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln
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ttg	aac	acg	tta	agt	atc	cgt	gca	gct	cag	ggc	gta	gac	cag	gat	tca	96
Leu	Asn	Thr	Leu	Ser	Ile	Arg	Ala	Ala	Gln	Gly	Val	Asp	Gln	Asp	Ser	
			20					25					30			
ctt	aag	ggt	tca	ctg	caa	acc	tac	ttc	gac	gcg	ctg	tac	gcc	aac	aat	144
Leu	Lys	Gly	Ser	Leu	Gln	Thr	Tyr	Phe	Asp	Ala	Leu	Tyr	Ala	Asn	Asn	
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Asp	Ser	His	His	Val	Ala	Met	Leu	Asp	Phe	Arg	Lys	Gln	Ile	Glu	Glu	
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Phe	Asn	Thr	Ile	Leu	Gly	Ala	Met	Ser	Leu	Gly	Ile	Ser	Ala	Ile	Gly	

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 Val Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu
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ggc gct cgt cga cgt gac att cgc ctg caa ttc gtc gtt gaa gcc atg 384
 Gly Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met
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atc att tgt ttc atc ggt ggc atc ctc ggc gtg ctt ttg ggc ggc att 432
 Ile Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile
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 165 170 175

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 Phe Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile
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Asp Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu
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Phe Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly
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Ile Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile
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Leu Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro
 145 150 155 160

Leu Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu
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 Met Ala Val Leu Phe
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 Ser Ile Met Gly Ala Leu Ile Leu Leu Val Leu Tyr Val Leu Phe Leu
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 Gly Lys Leu Gln Ile Asp Gly Leu Met Val Asp Leu Pro Asp Ser Ala
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cga gac gat gtt gaa gga ttc gtc ttc aat tgg gtg ttt tcc gga att 259
 Arg Asp Asp Val Glu Gly Phe Val Phe Asn Trp Val Phe Ser Gly Ile
 40 45 50

ctc atc acg tcc gca atc act gtt ccg caa gca gca ctt gga gtg ctg 307
 Leu Ile Thr Ser Ala Ile Thr Val Pro Gln Ala Ala Leu Gly Val Leu
 55 60 65

gtt gaa gat cgc acc cgc gga ggc atc aaa gat ttc ctc gtg gca ccc 355
 Val Glu Asp Arg Thr Arg Gly Gly Ile Lys Asp Phe Leu Val Ala Pro
 70 75 80 85

gta tcc aga acg acg ctg acg gtg tcc tat atc ttc gca gca gtc att 403
 Val Ser Arg Thr Thr Leu Thr Val Ser Tyr Ile Phe Ala Ala Val Ile
 90 95 100

gtc gcc atg acg att ttg atc ttt gaa atc gtg gtg gga agt att ggt 451
 Val Ala Met Thr Ile Leu Ile Phe Glu Ile Val Val Gly Ser Ile Gly
 105 110 115
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 Leu Ala Ile Leu Gly His Phe Ser Met Ser Ile Ala Arg Val Leu Glu
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 Leu Val Val Ala Leu Leu Leu Thr Leu Val Phe Ser Ala Ile Ala
 135 140 145
 gca ttt ctg atc acc ttg gtg aaa tct caa ggc gga atg tct gcg ctt 595
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 tca agc ctg gta ggc acc ctg gcg ggc ttt tta tct gct gct tat att 643
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 Pro Pro Ile Ala Leu Pro Glu Ala Val Thr Asn Val Leu Asn Phe Leu
 185 190 195
 ccg ttt acc cca gct gga atg ttg atc aga caa att gtg gtt gcc cca 739
 Pro Phe Thr Pro Ala Gly Met Leu Ile Arg Gln Ile Val Val Ala Pro
 200 205 210
 gca ttg gac gcg att tca ctt cca ccc gaa gcc ttc gat atc ttc caa 787
 Ala Leu Asp Ala Ile Ser Leu Pro Pro Glu Ala Phe Asp Ile Phe Gln
 215 220 225
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 Phe Gly Tyr Gly Leu Lys Leu Glu Met Phe Gly Glu Pro Val Ser Thr
 230 235 240 245
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 Trp Val Ala Val Gly Ile Val Ala Ser Trp Gly Val Val Phe Gly Leu
 250 255 260
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 Ile Ala Ala Phe Lys Met Lys Ser Val Val Arg
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 ttc 939

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<213> Corynebacterium glutamicum

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Leu Pro Asp Ser Ala Arg Asp Asp Val Glu Gly Phe Val Phe Asn Trp
 35 40 45

Val Phe Ser Gly Ile Leu Ile Thr Ser Ala Ile Thr Val Pro Gln Ala
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 Ala Leu Gly Val Leu Val Glu Asp Arg Thr Arg Gly Gly Ile Lys Asp
 65 70 75 80
 Phe Leu Val Ala Pro Val Ser Arg Thr Thr Leu Thr Val Ser Tyr Ile
 85 90 95
 Phe Ala Ala Val Ile Val Ala Met Thr Ile Leu Ile Phe Glu Ile Val
 100 105 110
 Val Gly Ser Ile Gly Leu Ala Ile Leu Gly His Phe Ser Met Ser Ile
 115 120 125
 Ala Arg Val Leu Glu Leu Val Val Ala Leu Leu Leu Leu Thr Leu Val
 130 135 140
 Phe Ser Ala Ile Ala Ala Phe Leu Ile Thr Leu Val Lys Ser Gln Gly
 145 150 155 160
 Gly Met Ser Ala Leu Ser Ser Leu Val Gly Thr Leu Ala Gly Phe Leu
 165 170 175
 Ser Ala Ala Tyr Ile Pro Pro Ile Ala Leu Pro Glu Ala Val Thr Asn
 180 185 190
 Val Leu Asn Phe Leu Pro Phe Thr Pro Ala Gly Met Leu Ile Arg Gln
 195 200 205
 Ile Val Val Ala Pro Ala Leu Asp Ala Ile Ser Leu Pro Pro Glu Ala
 210 215 220
 Phe Asp Ile Phe Gln Phe Gly Tyr Gly Leu Lys Leu Glu Met Phe Gly
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<212> DNA

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Ser	Asp	Glu	Gln	Ile	Glu	His	Ala	Ala	Arg	Leu	Ala	Gln	Ala	His	Asp		
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Phe	Ile	Asp	Arg	Leu	Pro	Asn	Lys	Tyr	Glu	Glu	Val	Ile	Gly	Glu	Arg		
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Gly	Leu	Thr	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala	Leu	Ala	Arg		
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Ala	Phe	Leu	Ala	His	Pro	Lys	Val	Leu	Val	Leu	Asp	Asp	Ala	Thr	Ser		
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Leu	Glu	Leu	Gly	Asp	Arg	Val	Gly	Leu	Val	Glu	Asp	Gly	Arg	Val	Thr		
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ctg	atg	gct	ctt	gat	ttc	cag	gat	tct	cac	gat	ccg	gaa	ttc	acc	ctc		547
Leu	Met	Ala	Leu	Asp	Phe	Gln	Asp	Ser	His	Asp	Pro	Glu	Phe	Thr	Leu		
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Gly	Met	Ser	Met	Pro	Ala	Thr	Pro	Glu	Leu	Leu	Ala	Gln	Ile	Glu	Ala		
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ctg	cca	gca	gca	acg	gaa	gaa	aca	cga	gtt	gat	gcc	ggg	agg	cta	cgc		739
Leu	Pro	Ala	Ala	Thr	Glu	Glu	Thr	Arg	Val	Asp	Ala	Gly	Arg	Leu	Arg		
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acc	agt	acc	tcc	ggt	ttc	aaa	ttg	ctc	agt	tta	ttc	aag	cag	gtc	cgt		787
Thr	Ser	Thr	Ser	Gly	Phe	Lys	Leu	Leu	Ser	Leu	Phe	Lys	Gln	Val	Arg		
	215					220					225						
tgg	ctc	gtc	gtc	gcg	gtc	atc	gcg	ttg	ttg	ctg	gtg	ggc	gta	gcc	gcc		835
Trp	Leu	Val	Val	Ala	Val	Ile	Ala	Leu	Leu	Leu	Val	Gly	Val	Ala	Ala		

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Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala Ile Asp Asn Gly Val	250	255	260	
caa gca caa agc acc tcc acg ttg tgg tgg atc gcc atc gca ggc agc				931
Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile Ala Ile Ala Gly Ser	265	270	275	
gta gta gtc ctt ctg tcc tgg gcc gcc gcc gcg atc aac acg att atc				979
Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile	280	285	290	
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Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser	295	300	305	
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Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr Phe Glu Arg Thr Met	310	315	320	325
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Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser	330	335	340	
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Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr	345	350	355	
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Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr Asp Ala Gln Leu Ala	360	365	370	
ctc gtt gcg ctg tcc gtg gtg ccg atc atc atc gtg ctc act ctc att				1267
Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile Val Leu Thr Leu Ile	375	380	385	
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Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala Ser Arg Glu Gln Ala	390	395	400	405
agc cag gtc aac gcg gta ttc cac gag tcc atc gcc ggt tta cgc acc				1363
Ser Gln Val Asn Ala Val Phe His Glu Ser Ile Ala Gly Leu Arg Thr	410	415	420	
gcg cag atg cac cgc atg gaa gac caa gtc ttt gac aat tat gcg ggc				1411
Ala Gln Met His Arg Met Glu Asp Gln Val Phe Asp Asn Tyr Ala Gly	425	430	435	
gaa gca gag gaa ttc cga cgc ctg cgt gtg aaa tcc cag acg gcc atc				1459
Glu Ala Glu Glu Phe Arg Arg Leu Arg Val Lys Ser Gln Thr Ala Ile	440	445	450	
gcc atc tac ttc ccc ggc ctt ggc gcg ctc tct gaa atc gcc cag gca				1507
Ala Ile Tyr Phe Pro Gly Leu Gly Ala Leu Ser Glu Ile Ala Gln Ala	455	460	465	
ctc gtc ctc ggt ttc ggc gca ctg caa gta acg cgc ggc gac atc tcc				1555
Leu Val Leu Gly Phe Gly Ala Leu Gln Val Thr Arg Gly Asp Ile Ser	470	475	480	485

Gly Leu Met Phe Gly Pro Ile Gln Gln Leu Ser Gln Ile Phe Asp Ser
 500 505 510

Tyr Gln Gln Ala Ala Val Gly Phe Arg Arg Ile Thr Glu Leu Leu Ala
 515 520 525

Thr Gln Pro Ser Val Gln Ile Trp Ala Pro Thr Gly Thr Leu Gly Arg
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Leu Pro Arg Ser Leu Tyr Cys Leu Thr Thr Ser Pro Ser Ala Ile Gln
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Thr Ile Arg Ser

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 Met Gly Leu Asp Val
 1 5

agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat 163
 Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp
 10 15 20

ttt atc gat cgc ctt cca aac aaa tac gag gaa gtc att ggc gaa cgc 211
 Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu Val Ile Gly Glu Arg
 25 30 35

ggc ctg acg ctt tct ggt ggt caa cgc caa cgc atc gcc ctc gca cgg 259
 Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Leu Ala Arg
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 Ala Phe Leu Ala His Pro Lys Val Leu Val Leu Asp Asp Ala Thr Ser
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 Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe Gln Ala Leu Arg Glu
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gaa ctg cac gat gtc acc att ttg atc atc gcg cac cgc cac tcc act 403
 Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala His Arg His Ser Thr
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Leu	Met	Ala	Leu	Asp	Phe	Gln	Asp	Ser	His	Asp	Pro	Glu	Phe	Thr	Leu	
	135					140					145					
gac	aac	ggt	tca	cta	ccc	agc	caa	gag	caa	ttg	tgg	ccg	gag	gtc	tcc	595
Asp	Asn	Gly	Ser	Leu	Pro	Ser	Gln	Glu	Gln	Leu	Trp	Pro	Glu	Val	Ser	
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aca	gaa	aag	cag	tac	aag	att	ctt	gcg	cct	gcc	cct	ggt	cga	ggc	cgt	643
Thr	Glu	Lys	Gln	Tyr	Lys	Ile	Leu	Ala	Pro	Ala	Pro	Gly	Arg	Gly	Arg	
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ggc	atg	tcc	atg	cca	gca	acc	cct	gag	ctg	ctc	gcc	cag	att	gag	gcg	691
Gly	Met	Ser	Met	Pro	Ala	Thr	Pro	Glu	Leu	Leu	Ala	Gln	Ile	Glu	Ala	
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ctg	cca	gca	gca	acg	gaa	gaa	aca	cga	gtt	gat	gcc	ggg	agg	cta	cgc	739
Leu	Pro	Ala	Ala	Thr	Glu	Glu	Thr	Arg	Val	Asp	Ala	Gly	Arg	Leu	Arg	
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acc	agt	acc	tcc	ggt	ttc	aaa	ttg	ctc	agt	tta	ttc	aag	cag	gtc	cgt	787
Thr	Ser	Thr	Ser	Gly	Phe	Lys	Leu	Leu	Ser	Leu	Phe	Lys	Gln	Val	Arg	
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tgg	ctc	gtc	gtc	gcg	gtc	atc	gcg	ttg	ttg	ctg	gtg	ggc	gta	gcc	gcc	835
Trp	Leu	Val	Val	Ala	Val	Ile	Ala	Leu	Leu	Leu	Val	Gly	Val	Ala	Ala	
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gat	cta	gca	ttt	cca	aca	ctg	atg	cgc	gca	gcc	atc	gac	aac	ggt	gtg	883
Asp	Leu	Ala	Phe	Pro	Thr	Leu	Met	Arg	Ala	Ala	Ile	Asp	Asn	Gly	Val	
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caa	gca	caa	agc	acc	tcc	acg	ttg	tgg	tgg	atc	gcc	atc	gca	ggc	agc	931
Gln	Ala	Gln	Ser	Thr	Ser	Thr	Leu	Trp	Trp	Ile	Ala	Ile	Ala	Gly	Ser	
			265					270					275			
gta	gta	gtc	ctt	ctg	tcc	tgg	gcc	gcc	gcc	gcg	atc	aac	acg	att	atc	979
Val	Val	Val	Leu	Leu	Ser	Trp	Ala	Ala	Ala	Ala	Ile	Asn	Thr	Ile	Ile	
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Phe	Val	His	Leu	Leu	Arg	Leu	Ser	Met	Ser	Tyr	Phe	Glu	Arg	Thr	Met	
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Ser	Gly	Arg	Ile	Met	Thr	Arg	Met	Thr	Thr	Asp	Ile	Asp	Asn	Leu	Ser	
				330					335					340		
tcc	ttc	ctc	caa	tca	ggt	ctg	gcg	caa	aca	gtt	gtc	tct	gtg	ggc	acg	1171
Ser	Phe	Leu	Gln	Ser	Gly	Leu	Ala	Gln	Thr	Val	Val	Ser	Val	Gly	Thr	
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G E E S S - P H E S E S S

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Val Ile Gly Glu Arg Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg
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Ile Ala Leu Ala Arg Ala Phe Leu Ala His Pro Lys Val Leu Val Leu
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Asp Asp Ala Thr Ser Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe
  65          70          75          80
Gln Ala Leu Arg Glu Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala
          85          90          95
His Arg His Ser Thr Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu
          100          105          110
Asp Gly Arg Val Thr Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His
      115          120          125
Ala Arg Phe Ser His Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp
      130          135          140
Pro Glu Phe Thr Leu Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu
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Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala
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 Ala Gln Ile Glu Ala Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp
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 Val Gly Val Ala Ala Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala
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 Val Ser Val Gly Thr Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr
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 Val Leu Thr Leu Ile Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala
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 Ser Arg Glu Gln Ala Ser Gln Val Asn Ala Val Phe His Glu Ser Ile
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Val Ser Leu Leu Asp His Pro Glu Ser Leu Pro Gly Tyr Leu Ser Ser
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Leu Ala Ile Val Glu Tyr Leu His Glu Gln Pro Leu Glu Phe Arg Ala
25 30 35

ccg att act gtg att act ggt gaa aat ggg gtg ggt aaa tcc acg ttg 259
Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val Gly Lys Ser Thr Leu
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ggt gag gct ttg gcg gtg ggg atg cgc ctt aat ccg tct ggt ggc tct 307
Val Glu Ala Leu Ala Val Gly Met Arg Leu Asn Pro Ser Gly Gly Ser
55 60 65

agg cat gca aac ttt ggc agg gaa ggc gat att gtg tcg tcg ctt cat 355
Arg His Ala Asn Phe Gly Arg Glu Gly Asp Ile Val Ser Ser Leu His
70 75 80 85

cag tcg ttg aag ttg gtg cgg aga gaa aac cct cgg gat gcg ttc ttt 403
Gln Ser Leu Lys Leu Val Arg Arg Glu Asn Pro Arg Asp Ala Phe Phe
90 95 100

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Phe Arg Gly Glu Thr Met Tyr Asn Val Ala Ser Tyr Tyr Glu Glu Leu
105 110 115

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Met Gly Glu Lys Asn Met His Asp Leu His Lys Met Ser His Gly Glu
120 125 130

tcg gta ttt gcg gtg att gat cgg cgt ttt aac aat caa gga ttt ttt 547
Ser Val Phe Ala Val Ile Asp Arg Arg Phe Asn Asn Gln Gly Phe Phe
135 140 145

gtt ttg gac gag cct gag gca ggc ctt tcc atg ctg agg cag ttg gag 595
Val Leu Asp Glu Pro Glu Ala Gly Leu Ser Met Leu Arg Gln Leu Glu
150 155 160 165

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Leu	Leu	Gly	Lys	Leu	Gly	Asn	Leu	Ala	Arg	Gly	Gly	Ala	Gln	Ile	Ile	
				170					175					180		

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Met Ala Thr His Ser Pro Ile Leu Leu Ala Ile Pro Gly Ala Glu Ile	
185	190
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Leu Glu Ile Thr Ser Ser Gly Val Ala Lys Val Asn Phe Glu Asp Ala

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gag gct gtt cgt gcg gct cgg gaa ttt gtg gca gat ccg cga ggt acg 787
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Gly Lys Ser Thr Leu Val Glu Ala Leu Ala Val Gly Met Arg Leu Asn
 50 55 60

Pro Ser Gly Gly Ser Arg His Ala Asn Phe Gly Arg Glu Gly Asp Ile
 65 70 75 80

Val Ser Ser Leu His Gln Ser Leu Lys Leu Val Arg Arg Glu Asn Pro
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Arg Asp Ala Phe Phe Phe Arg Gly Glu Thr Met Tyr Asn Val Ala Ser
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Tyr Tyr Glu Glu Leu Met Gly Glu Lys Asn Met His Asp Leu His Lys
 115 120 125

Met Ser His Gly Glu Ser Val Phe Ala Val Ile Asp Arg Arg Phe Asn
 130 135 140

Asn Gln Gly Phe Phe Val Leu Asp Glu Pro Glu Ala Gly Leu Ser Met
 145 150 155 160

Leu Arg Gln Leu Glu Leu Leu Gly Lys Leu Gly Asn Leu Ala Arg Gly
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Gly Ala Gln Ile Ile Met Ala Thr His Ser Pro Ile Leu Leu Ala Ile
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Asn Phe Glu Asp Ala Glu Ala Val Arg Ala Ala Arg Glu Phe Val Ala
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Met Thr Glu Thr Leu
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 Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln
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tat gag gaa ttt gcg gaa aag aag aag gac ctt gtg gca cgt gct cga 931
 Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg
 265 270 275

acg cag cgt gaa tgg tct agt cac ggt gtc cgc aat gct att aaa cgt 979
 Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg Asn Ala Ile Lys Arg
 280 285 290

gca cct gac aac gac aaa ctt cgg aag aaa gcc gct gcg gaa tcc agt 1027
 Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala Ala Ala Glu Ser Ser
 295 300 305

gaa aag cag gct caa aaa gtc cgc cag atg gaa agc cgc atc gct cgg 1075
 Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu Ser Arg Ile Ala Arg
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 Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly Pro Asn Gly Ala Gly
 375 380 385

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 410 415 420

gca cga gcg tta ctt gat cca cag ttg cca ctg att tct gcg ttt gaa 1411
 Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu Ile Ser Ala Phe Glu
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 Lys His Val Pro Asp Leu Pro Ile Ser Glu Val Arg Thr Leu Leu Ala
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ggc gtc aac gtg ctt gtt ctt gat gag ccc acc aac cac ctt gac ctg 1603

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225					230					235					240
Gly	Gly	Gly	Tyr	Asp	Ser	Tyr	Leu	Glu	Glu	Arg	Ala	Val	Leu	Arg	Gln
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His	Ala	Arg	Asp	Gln	Tyr	Glu	Glu	Phe	Ala	Glu	Lys	Lys	Lys	Asp	Leu
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Val	Ala	Arg	Ala	Arg	Thr	Gln	Arg	Glu	Trp	Ser	Ser	His	Gly	Val	Arg
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Asn	Ala	Ile	Lys	Arg	Ala	Pro	Asp	Asn	Asp	Lys	Leu	Arg	Lys	Lys	Ala
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Ala	Ala	Glu	Ser	Ser	Glu	Lys	Gln	Ala	Gln	Lys	Val	Arg	Gln	Met	Glu
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Ser	Arg	Ile	Ala	Arg	Leu	Glu	Glu	Val	Glu	Glu	Pro	Arg	Lys	Glu	Trp
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Lys	Leu	Gln	Phe	Ser	Val	Gly	Lys	Ala	Ser	Arg	Ser	Ser	Ser	Val	Val
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Ser	Thr	Leu	Asn	Asp	Ala	Ser	Phe	Thr	Gln	Gly	Asp	Phe	Thr	Leu	Gly
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Pro	Val	Ser	Ile	Gln	Val	Asn	Ala	Gly	Asp	Arg	Ile	Gly	Ile	Thr	Gly
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Pro	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Leu	Arg	Gly	Leu	Leu	Gly	Asn
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Gln	Glu	Pro	Thr	Ser	Gly	Thr	Ala	Thr	Met	Gly	Thr	Ser	Val	Ala	Ile
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Gly	Glu	Ile	Asp	Gln	Ala	Arg	Ala	Leu	Leu	Asp	Pro	Gln	Leu	Pro	Leu
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Ile	Ser	Ala	Phe	Glu	Lys	His	Val	Pro	Asp	Leu	Pro	Ile	Ser	Glu	Val
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Arg	Thr	Leu	Leu	Ala	Lys	Phe	Gly	Leu	Asn	Asp	Asn	His	Val	Glu	Arg
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Asn	His	Leu	Asp	Leu	Glu	Ala	Ile	Glu	Gln	Leu	Glu	Gln	Ala	Leu	Ala
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Ser	Tyr	Asp	Gly	Val	Leu	Leu	Leu	Val	Thr	His	Asp	Arg	Arg	Met	Leu
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 185 190 195

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 200 205 210

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 230 235 240 245

tac cgg atg tct tcg tta atg cgg ttg aag gcg ctg ctc ttc aag agg 883
 Tyr Arg Met Ser Ser Leu Met Arg Leu Lys Ala Leu Leu Phe Lys Arg
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ggt cac tat ctt ggt tgg gtg cgt ccg aag gcc ata gcg aag gcc aaa 931
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cta 981

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<212> PRT

<213> Corynebacterium glutamicum

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Ala Ile Tyr Gly Ile Val Gly Pro Asn Gly Ala Gly Lys Thr Thr Met
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Leu Ser Met Ala Thr Gly Leu Leu Arg Pro Asn Lys Gly Thr Ala Trp
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Ile Ser Gly Phe Asn Val Trp Glu Glu Pro Asn Asp Ala Lys Arg Ser

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Glu	Ala	Ala	Gly	Lys	Arg	Val	Val	Asp	Tyr	Ser	Ala	Gly	Met	Thr	Lys				
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Lys	Ile	Leu	Leu	Ala	Gln	Ala	Leu	Ile	His	Asn	Pro	Lys	Val	Leu	Ile				
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Variable	Mean	SD	Min	Max
Age	35.5	10.5	20	65
Gender	Male	0.75	0	1
Marital Status	Married	0.65	0	1
Education	High School	0.15	0	1
Occupation	Manager	0.25	0	1
Income	\$30,000	\$15,000	\$10,000	\$50,000
Health	Good	0.85	0	1
Stress	Low	0.25	0	1
Life Satisfaction	High	0.75	0	1
Work-Life Balance	Good	0.65	0	1
Job Satisfaction	High	0.75	0	1
Organizational Commitment	High	0.75	0	1
Turnover Intent	Low	0.15	0	1
Engagement	High	0.75	0	1
Productivity	High	0.75	0	1
Teamwork	High	0.75	0	1
Communication	High	0.75	0	1
Conflict Resolution	High	0.75	0	1
Leadership	High	0.75	0	1
Innovation	High	0.75	0	1
Adaptability	High	0.75	0	1
Resilience	High	0.75	0	1
Optimism	High	0.75	0	1
Empathy	High	0.75	0	1
Emotional Stability	High	0.75	0	1
Conscientiousness	High	0.75	0	1
Openness	High	0.75	0	1
Agreeableness	High	0.75	0	1
Neuroticism	Low	0.15	0	1
Extraversion	High	0.75	0	1
Conscientiousness	High	0.75	0	1
Openness	High	0.75	0	1
Agreeableness	High	0.75	0	1
Neuroticism	Low	0.15	0	1
Extraversion	High	0.75	0	1
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66250-46260980

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 Gly Val Lys Val Ala Met Ile Thr Gly Asp Ala Thr Gln Val Ala Gln
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gca gtg ggc aag gat ctg ggg atc gat gag gtc ttc gcc gag gtt ctg 1843
 Ala Val Gly Lys Asp Leu Gly Ile Asp Glu Val Phe Ala Glu Val Leu
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ccg cag gac aag gac acc aag gtc acc cag ctg cag gag cgc ggt ctg 1891
 Pro Gln Asp Lys Asp Thr Lys Val Thr Gln Leu Gln Glu Arg Gly Leu
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agc gtg gcc atg gtc ggc gac ggt gtc aat gac gcc ccg gcc ctg gcc 1939
 Ser Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala
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cgg gcc gag gtc ggt att gcg att ggc gcg ggt aca gat gtg gcg atg 1987
 Arg Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met
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gag tcc gcc ggg gtg gtc ctg gcc agt gat gat ccc cgg gcc gtg ctg 2035
 Glu Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu
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tcg atg atc gag ctc tcc cat gcc agc tac cgc aag atg gtc cag aac 2083
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 Leu Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala
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ggt gtg ctc gcc cct atc ggt gtg ctg ctt ccc ccg gcg gcg gcc gcc 2179
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atc ttg atg tcc ctg tcc acg atc atc gtc gcc ctc aac gcc cag ctg 2227
 Ile Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu
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cta cgc cgg atc gac ctg gac ccg gct cac cta gct ccg acc gac ggg 2275
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735

2340

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Pro	Val	Val	Phe	Phe	Ser	Pro	Met	Phe	Ala	Asp	Leu	Leu	Gly	Tyr	Asn
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Ile	Pro	Glu	Ile	Pro	Gly	Ala	Tyr	Trp	Ile	Pro	Pro	Val	Leu	Gly	Thr
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Ile	Thr	Val	Ala	Phe	Ile	Ala	Ser	Trp	Val	Thr	Thr	Leu	Gly	Leu	Gly
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Gly	Phe	His	Leu	Asp	Phe	Trp	Trp	Glu	Leu	Ala	Leu	Leu	Val	Thr	Ile
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Met	Leu	Leu	Gly	His	Trp	Leu	Glu	Met	Arg	Ala	Leu	Gly	Ala	Ala	Ser
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Ser	Ala	Leu	Asp	Ala	Leu	Ala	Ala	Leu	Leu	Pro	Asp	Glu	Ala	Glu	Lys
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Asp	Asp	Val	Val	Leu	Val	Arg	Ala	Gly	Ala	Arg	Val	Pro	Ala	Asp	Gly
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Thr	Ile	Ile	Asp	Gly	Ala	Ala	Glu	Phe	Asp	Glu	Ala	Met	Ile	Thr	Gly
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Glu	Ser	Arg	Pro	Val	Tyr	Arg	Asp	Thr	Gly	Glu	Thr	Val	Val	Ala	Gly
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 Gly Asp Thr Ala Leu Ala Gly Ile Gln Arg Met Val Ala Asp Ala Gln
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 Leu Phe Trp Phe Ala Leu Ile Thr Ala Leu Ile Thr Ala Val Val Trp
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 Thr Ile Ile Gly Ser Pro Asp Asp Ala Val Val Arg Ala Val Thr Val
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 Ala Pro Ala Thr Gly Ile Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala
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 Ala Ala Glu Ala Asp Ser Glu His Pro Val Ala Arg Ala Ile Val Thr
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 485 490 495
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 Gly Ala Gly Val Leu His Val Val Arg Asp Gly Glu Ile Ile Gly Ala
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 Val Ala Val Glu Asp Lys Ile Arg Pro Glu Ser Arg Ala Ala Val Arg
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 Ala Leu Gln Ala Arg Gly Val Lys Val Ala Met Ile Thr Gly Asp Ala
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 Thr Gln Val Ala Gln Ala Val Gly Lys Asp Leu Gly Ile Asp Glu Val
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 Phe Ala Glu Val Leu Pro Gln Asp Lys Asp Thr Lys Val Thr Gln Leu
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Gln Glu Arg Gly Leu Ser Val Ala Met Val Gly Asp Gly Val Asn Asp
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 Ala Pro Ala Leu Ala Arg Ala Glu Val Gly Ile Ala Ile Gly Ala Gly
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 Thr Asp Val Ala Met Glu Ser Ala Gly Val Val Leu Ala Ser Asp Asp
 625 630 635 640
 Pro Arg Ala Val Leu Ser Met Ile Glu Leu Ser His Ala Ser Tyr Arg
 645 650 655
 Lys Met Val Gln Asn Leu Val Trp Ala Thr Gly Tyr Asn Ile Val Ala
 660 665 670
 Val Pro Leu Ala Ala Gly Val Leu Ala Pro Ile Gly Val Leu Leu Pro
 675 680 685
 Pro Ala Ala Ala Ala Ile Leu Met Ser Leu Ser Thr Ile Ile Val Ala
 690 695 700
 Leu Asn Ala Gln Leu Leu Arg Arg Ile Asp Leu Asp Pro Ala His Leu
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 Pro Val Arg

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 <213> Corynebacterium glutamicum

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 <222> (50)..(1285)
 <223> RXN00939

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 ggc gtc atg atc gcc gcc ctg gcc gtc ggc ctg atc acc ctg aac gtt 154
 Gly Val Met Ile Ala Ala Leu Ala Val Gly Leu Ile Thr Leu Asn Val
 20 25 30 35
 gaa ctg gcc ctg acc ctg ctg gtc atc gcc tgc ccg ggt gcc ctg gtc 202
 Glu Leu Ala Leu Thr Leu Leu Val Ile Ala Cys Pro Gly Ala Leu Val
 40 45 50
 atc tcg atc ccg gtc tcg atc gtc gcc ggt atc ggc cgc tcc gcc aag 250
 Ile Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg Ser Ala Lys
 55 60 65

G E E S S T E C T E D

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gtc gac acc gta gtc gtc gac aag acc ggc acc ctg acc aac ggc cgc 346
 Val Asp Thr Val Val Val Asp Lys Thr Gly Thr Leu Thr Asn Gly Arg
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ccc gag ctg acc aac gtc gac gtc ctt gac ccc gcc tac tcg gac gat 394
 Pro Glu Leu Thr Asn Val Asp Val Leu Asp Pro Ala Tyr Ser Asp Asp
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gag gtg ctc acc ctg gcc gcc cgc gcg gaa acc gcc tcc gag cac ccc 442
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ctg gcc gag gcc atc atc cgc ggc gcg gag aac agg ggc ttg acc gtg 490
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 135 140 145

gcg atg gta gaa aag gcc gaa ccg gtc gcc ggc cgc ggc atc cgc gct 538
 Ala Met Val Glu Lys Ala Glu Pro Val Ala Gly Arg Gly Ile Arg Ala
 150 155 160

gac gtg gac ggt gcc acc gtg gcc gtg ggc tca gcc gac ctg ctc gat 586
 Asp Val Asp Gly Ala Thr Val Ala Val Gly Ser Ala Asp Leu Leu Asp
 165 170 175

cac acc ccg gat aac acc cgc att ctc gag ctc aac gaa cag ggc agg 634
 His Thr Pro Asp Asn Thr Arg Ile Leu Glu Leu Asn Glu Gln Gly Arg
 180 185 190 195

acc gcc atg tac gtc ggc atc aac ggc aag gcc gtg ggc atc gtc gct 682
 Thr Ala Met Tyr Val Gly Ile Asn Gly Lys Ala Val Gly Ile Val Ala
 200 205 210

gtg gcc gac acc atc cga gat gat gcc ccg gcc gcg atc agg tcc ctg 730
 Val Ala Asp Thr Ile Arg Asp Asp Ala Pro Ala Ala Ile Arg Ser Leu
 215 220 225

cac aat aag gga atc cgc gtg gtc atg gcc acc ggt gat gcc gaa cgc 778
 His Asn Lys Gly Ile Arg Val Val Met Ala Thr Gly Asp Ala Glu Arg
 230 235 240

gtc gcc cgc aac gtc gcc gcc gag ctc ggt gtc gat gag gtg agg gca 826
 Val Ala Arg Asn Val Ala Ala Glu Leu Gly Val Asp Glu Val Arg Ala
 245 250 255

gaa ctg atg cct gag gac aag ctc gag atc gtc aag gag ctg cag gcg 874
 Glu Leu Met Pro Glu Asp Lys Leu Glu Ile Val Lys Glu Leu Gln Ala
 260 265 270 275

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 Gln Gly Arg Val Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro
 280 285 290

gca ctg gcc acc gcg gac atc ggt gtg gcg atg ggt gcg gcc ggt tcg 970
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 295 300 305

Glu His Pro Leu Ala Glu Ala Ile Ile Arg Gly Ala Glu Asn Arg Gly
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 145 150 155 160
 Ile Arg Ala Asp Val Asp Gly Ala Thr Val Ala Val Gly Ser Ala Asp
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 Leu Leu Asp His Thr Pro Asp Asn Thr Arg Ile Leu Glu Leu Asn Glu
 180 185 190
 Gln Gly Arg Thr Ala Met Tyr Val Gly Ile Asn Gly Lys Ala Val Gly
 195 200 205
 Ile Val Ala Val Ala Asp Thr Ile Arg Asp Asp Ala Pro Ala Ala Ile
 210 215 220
 Arg Ser Leu His Asn Lys Gly Ile Arg Val Val Met Ala Thr Gly Asp
 225 230 235 240
 Ala Glu Arg Val Ala Arg Asn Val Ala Ala Glu Leu Gly Val Asp Glu
 245 250 255
 Val Arg Ala Glu Leu Met Pro Glu Asp Lys Leu Glu Ile Val Lys Glu
 260 265 270
 Leu Gln Ala Gln Gly Arg Val Val Ala Met Val Gly Asp Gly Val Asn
 275 280 285
 Asp Thr Pro Ala Leu Ala Thr Ala Asp Ile Gly Val Ala Met Gly Ala
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 Ala Gly Ser Pro Ala Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala
 305 310 315 320
 Asp Lys Leu Pro Arg Leu Pro Tyr Ala Leu Gly Leu Ala Gln Arg Thr
 325 330 335
 Val Arg Thr Met Arg Val Asn Ile Gly Ile Ala Leu Leu Thr Val Thr
 340 345 350
 Ile Leu Leu Ala Gly Val Leu Leu Gly Gly Val Thr Met Ser Ile Gly
 355 360 365
 Met Leu Val His Glu Ala Ser Val Leu Leu Val Ile Ala Ile Ala Met
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ccc acc ctg aag gaa gac aag gac aag gca gac gtc agt act gct gac 144
Pro Thr Leu Lys Glu Asp Lys Asp Lys Ala Asp Val Ser Thr Ala Asp
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Met Ala Gln Thr Pro
                1                      5

gcc aaa atc ccg gcg gca ctg aat ttc att gac gtc gac ctc ggc gtt 163
Ala Lys Ile Pro Ala Ala Leu Asn Phe Ile Asp Val Asp Leu Gly Val
                10                      15                      20

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Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn Tyr Ala Thr Glu Ser	
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gca cag gtc agc tac gac ccc tca aag gtc agc cct gaa cag ctg att	307
Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser Pro Glu Gln Leu Ile	
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aag act gtt gag gac acc ggc tac ggt gct ttc acg atg gct tcc gca	355
Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe Thr Met Ala Ser Ala	
70 75 80 85	
gct gcc gaa tca gaa gag gac aac gct cca gct gac agc ggc cag tcc	403
Ala Ala Glu Ser Glu Glu Asp Asn Ala Pro Ala Asp Ser Gly Gln Ser	
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cgc atc gac gca gct cgc gac cac gaa gca gcc gac ctg aaa cac cgc	451
Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala Asp Leu Lys His Arg	
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Val Ile Val Ser Ala Leu Leu Ser Val Pro Val Val Leu Val Ser Met	
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Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp Ala Val Leu Thr Leu	
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Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro Phe His Lys Ala Thr	
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Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met Asn Thr Leu Val Ser	
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Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu Trp Ala Leu Phe Ile	
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Glu Asn Ala Gly His Pro Gly Met Lys Met Glu Met His Leu Leu Pro	
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215 220 225	
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Ile Thr Phe Leu Leu Leu Gly Arg Trp Phe Glu Thr Lys Ala Lys Gly	
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Gln Ser Ser Glu Ala Leu Arg Lys Leu Leu Asp Met Gly Ala Lys Asp	
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Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala Val Asp Glu Ser Met	
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Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr Lys Gly Ser Lys Val	
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Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu Met Val Lys Val Thr	
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Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met Ala Lys Leu Val Thr	
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Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro Cys Ala Leu Gly Leu	
410 415 420	
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Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val Thr Thr Gly Thr Met	
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Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser Glu Thr Glu Ile Leu	
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Glu Phe Ala Ala Val Glu Ser Ala Ser Glu His Pro Ile Ala Gln	
490 495 500	
gca atc gcc aag gcc gcc gaa cac gag caa gtc acc gac ttc caa aac	1651

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Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala Leu Leu His Pro Phe	
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Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val Val Val Thr Ile Asp	
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Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp Thr Val Lys Asp Thr	
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tcc gcc gaa gca atc cgc gga ctc aag gaa ctg gga ctc acc cca atc	1891
Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu Gly Leu Thr Pro Ile	
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Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys Ser Val Ala Ala Glu	
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gtc ggc atc gac caa gtc atc gcc aac gtc ctc ccc cac gaa aaa gtc	1987
Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu Pro His Glu Lys Val	
615 620 625	
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Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys Asn Val Ala Met Val	
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ggc gac ggc gtc aac gat gcc gca gct ctt gcc caa gct gac ctc gga	2083
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ctc gcc atg gga gcc ggc acc gac gta gcc atc gaa gcc tcc gac atc	2131
Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile Glu Ala Ser Asp Ile	
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Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val Asp Ala Ile Arg Leu	
680 685 690	
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Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn Leu Phe Trp Ala Phe	
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Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser Ser Val Phe Val Val	
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745

750

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2388

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Pro	Glu	Gln	Leu	Ile	Lys	Thr	Val	Glu	Asp	Thr	Gly	Tyr	Gly	Ala	Phe
	65				70					75					80

Thr	Met	Ala	Ser	Ala	Ala	Ala	Glu	Ser	Glu	Glu	Asp	Asn	Ala	Pro	Ala
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Asp	Ser	Gly	Gln	Ser	Arg	Ile	Asp	Ala	Ala	Arg	Asp	His	Glu	Ala	Ala
		100						105					110		

Asp	Leu	Lys	His	Arg	Val	Ile	Val	Ser	Ala	Leu	Leu	Ser	Val	Pro	Val
		115					120					125			

Val	Leu	Val	Ser	Met	Ile	Pro	Ala	Leu	Gln	Phe	Asn	Asn	Trp	Gln	Trp
	130					135						140			

Ala	Val	Leu	Thr	Leu	Val	Thr	Pro	Ile	Phe	Phe	Trp	Gly	Gly	Ser	Pro
	145				150					155					160

Phe	His	Lys	Ala	Thr	Trp	Ala	Asn	Leu	Lys	Arg	Gly	Ser	Phe	Thr	Met
				165					170					175	

Asn	Thr	Leu	Val	Ser	Leu	Gly	Thr	Ser	Ala	Ala	Asp	Leu	Trp	Ser	Leu
		180						185					190		

Trp	Ala	Leu	Phe	Ile	Glu	Asn	Ala	Gly	His	Pro	Gly	Met	Lys	Met	Glu
		195					200					205			

Met	His	Leu	Leu	Pro	Ser	Ala	Ser	Thr	Met	Asp	Glu	Ile	Tyr	Leu	Glu
	210					215					220				

Thr	Val	Ala	Val	Val	Ile	Thr	Phe	Leu	Leu	Leu	Gly	Arg	Trp	Phe	Glu
	225				230					235					240

Thr	Lys	Ala	Lys	Gly	Gln	Ser	Ser	Glu	Ala	Leu	Arg	Lys	Leu	Leu	Asp
				245					250					255	

Met	Gly	Ala	Lys	Asp	Ala	Val	Val	Leu	Arg	Asp	Gly	Ala	Glu	Val	Arg
			260					265					270		

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Val Pro Val Asn Gln Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro
 275 280 285
 Gly Glu Lys Ile Ala Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala
 290 295 300
 Val Asp Glu Ser Met Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr
 305 310 315 320
 Lys Gly Ser Lys Val Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu
 325 330 335
 Met Val Lys Val Thr Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met
 340 345 350
 Ala Lys Leu Val Thr Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg
 355 360 365
 Leu Val Asp Gln Ile Ser Gln Val Phe Val Pro Val Val Ile Val Ile
 370 375 380
 Ala Ile Ala Thr Leu Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu
 385 390 395 400
 Ala Pro Ala Phe Thr Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro
 405 410 415
 Cys Ala Leu Gly Leu Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly
 420 425 430
 Arg Gly Ala Gln Leu Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu
 435 440 445
 Ser Thr Lys Lys Val Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val
 450 455 460
 Thr Thr Gly Thr Met Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser
 465 470 475 480
 Glu Thr Glu Ile Leu Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu
 485 490 495
 His Pro Ile Ala Gln Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val
 500 505 510
 Thr Asp Phe Gln Asn Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg
 515 520 525
 Gly His Glu Val Arg Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala
 530 535 540
 Leu Leu His Pro Phe Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val
 545 550 555 560
 Val Val Thr Ile Asp Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp
 565 570 575
 Thr Val Lys Asp Thr Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu
 580 585 590

acc gac ggt gaa gtc gac gaa ggt tcc tcc gca gtc gac gaa tcc atg 1027
 Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala Val Asp Glu Ser Met
 295 300 305

ctc acc ggc gaa tcc atc ccc gtt gaa gtc acc aag ggc tcc aaa gtt 1075
 Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr Lys Gly Ser Lys Val
 310 315 320 325

acc ggc gca acg ctg aac act tcc ggc cgc ctc atg gtg aaa gta acc 1123
 Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu Met Val Lys Val Thr
 330 335 340

cgc atc ggc gcc gac acc acc ctg tcg caa atg gct aaa ctg gtc acg 1171
 Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met Ala Lys Leu Val Thr
 345 350 355

gac gca cag tcc aaa aag gcc cct gtc cag cgt ctt gtt gac caa atc 1219
 Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg Leu Val Asp Gln Ile
 360 365 370

tcg cag gtt ttc gtt ccc gtt gtc atc gta att gct att gcg acg ctg 1267
 Ser Gln Val Phe Val Pro Val Val Ile Val Ile Ala Ile Ala Thr Leu
 375 380 385

atc gcg cac ctc gtc ttc acc gac gcc ggc ctc gcc cca gca ttc acc 1315
 Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu Ala Pro Ala Phe Thr
 390 395 400 405

gca gca gtc gcc gtc ctc att atc gcc tgc cct tgt gcc ctc ggc ctg 1363
 Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro Cys Ala Leu Gly Leu
 410 415 420

gca acc cca acc gca ctt ctg gtc gga acc ggc cgc ggc gcg caa ctt 1411
 Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly Arg Gly Ala Gln Leu
 425 430 435

ggt ctg ttg atc aag ggc cct gaa atc ctc gaa tcc acc aaa aaa gtc 1459
 Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu Ser Thr Lys Lys Val
 440 445 450

gac acc atc gtc ctc gac aaa acc ggc acc gtc acc acc ggc acc atg 1507
 Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val Thr Thr Gly Thr Met
 455 460 465

tcc gtc acc gac gtc acc gcc atc aac tac agc gaa acc gaa atc ctc 1555
 Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser Glu Thr Glu Ile Leu
 470 475 480 485

gaa ttc gct gca gcc gtc gag tcc gcc tcc gaa cac ccc atc gcc cag 1603
 Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu His Pro Ile Ala Gln
 490 495 500

gca atc gcc aag gcc gcc gaa cac gag caa gtc acc gac ttc caa aac 1651
 Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val Thr Asp Phe Gln Asn
 505 510 515

acc gca ggt cag gaa gtc acc ggt gta gtc cgc gga cac gag gtc cgc 1699
 Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg Gly His Glu Val Arg
 520 525 530

gtg ggc agg cct tca agc acg ctt atc gac gcc ctc ctc cac ccc ttc	1747
Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala Leu Leu His Pro Phe	
535 540 545	
caa cac gcc caa aaa atc ggc gga acc ccc gta gtc gtc acg att gac	1795
Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val Val Val Thr Ile Asp	
550 555 560 565	
ggc gta gat tcc gga ata atc acg gtc cgc gac acc gtc aaa gac acc	1843
Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp Thr Val Lys Asp Thr	
570 575 580	
tcc gcc gaa gca atc cgc gga ctc aag gaa ctg gga ctc acc cca atc	1891
Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu Gly Leu Thr Pro Ile	
585 590 595	
cta ctc acc gga gac aat gaa ggc gca gct aaa tcc gta gcc gct gaa	1939
Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys Ser Val Ala Ala Glu	
600 605 610	
gtc ggc atc gac caa gtc atc gcc aac gtc ctc ccc cac gaa aaa gtc	1987
Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu Pro His Glu Lys Val	
615 620 625	
caa aac gta gaa gcc ctc caa gca caa ggc aaa aac gtt gcg atg gtc	2035
Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys Asn Val Ala Met Val	
630 635 640 645	
ggc gac ggc gtc aac gat gcc gca gct ctt gcc caa gct gac ctc gga	2083
Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala Gln Ala Asp Leu Gly	
650 655 660	
ctc gcc atg gga gcc ggc acc gac gta gcc atc gaa gcc tcc gac atc	2131
Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile Glu Ala Ser Asp Ile	
665 670 675	
acc ctc atg aac aac gac ctc cga tcc gca gtc gac gcc atc cga ctg	2179
Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val Asp Ala Ile Arg Leu	
680 685 690	
tcc cgt aaa acc ctc ggc acc atc aag gga aac ctt ttc tgg gct ttc	2227
Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn Leu Phe Trp Ala Phe	
695 700 705	
gcc tac aat gtt gca cta atc cca gta gcg gcg atc gga ctc ctc aac	2275
Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala Ile Gly Leu Leu Asn	
710 715 720 725	
cca atg ctt gcc ggc att gcg atg gcc ttc agt tca gtt ttc gtc gtc	2323
Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser Ser Val Phe Val Val	
730 735 740	
tcc aat tcc ttg cgt ctg cga gga ttc aaa gca agg agc aac	2365
Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala Arg Ser Asn	
745 750 755	
taatgtccaa cagcgaatgc cac	2388

<210> 102

<211> 755

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 102

Met	Ala	Gln	Thr	Pro	Ala	Lys	Ile	Pro	Ala	Ala	Leu	Asn	Phe	Ile	Asp	1	5	10	15
Val	Asp	Leu	Gly	Val	Thr	Gly	Met	Thr	Cys	Thr	Ser	Cys	Ser	Ala	Arg	20	25	30	
Val	Glu	Arg	Lys	Leu	Asn	Lys	Leu	Asp	Gly	Val	Glu	Ala	Thr	Val	Asn	35	40	45	
Tyr	Ala	Thr	Glu	Ser	Ala	Gln	Val	Ser	Tyr	Asp	Pro	Ser	Lys	Val	Ser	50	55	60	
Pro	Glu	Gln	Leu	Ile	Lys	Thr	Val	Glu	Asp	Thr	Gly	Tyr	Gly	Ala	Phe	65	70	75	80
Thr	Met	Ala	Ser	Ala	Ala	Ala	Glu	Ser	Glu	Glu	Asp	Asn	Ala	Pro	Ala	85	90	95	
Asp	Ser	Gly	Gln	Ser	Arg	Ile	Asp	Ala	Ala	Arg	Asp	His	Glu	Ala	Ala	100	105	110	
Asp	Leu	Lys	His	Arg	Val	Ile	Val	Ser	Ala	Leu	Leu	Ser	Val	Pro	Val	115	120	125	
Val	Leu	Val	Ser	Met	Ile	Pro	Ala	Leu	Gln	Phe	Asn	Asn	Trp	Gln	Trp	130	135	140	
Ala	Val	Leu	Thr	Leu	Val	Thr	Pro	Ile	Phe	Phe	Trp	Gly	Gly	Ser	Pro	145	150	155	160
Phe	His	Lys	Ala	Thr	Trp	Ala	Asn	Leu	Lys	Arg	Gly	Ser	Phe	Thr	Met	165	170	175	
Asn	Thr	Leu	Val	Ser	Leu	Gly	Thr	Ser	Ala	Ala	Asp	Leu	Trp	Ser	Leu	180	185	190	
Trp	Ala	Leu	Phe	Ile	Glu	Asn	Ala	Gly	His	Pro	Gly	Met	Lys	Met	Glu	195	200	205	
Met	His	Leu	Leu	Pro	Ser	Ala	Ser	Thr	Met	Asp	Glu	Ile	Tyr	Leu	Glu	210	215	220	
Thr	Val	Ala	Val	Val	Ile	Thr	Phe	Leu	Leu	Leu	Gly	Arg	Trp	Phe	Glu	225	230	235	240
Thr	Lys	Ala	Lys	Gly	Gln	Ser	Ser	Glu	Ala	Leu	Arg	Lys	Leu	Leu	Asp	245	250	255	
Met	Gly	Ala	Lys	Asp	Ala	Val	Val	Leu	Arg	Asp	Gly	Ala	Glu	Val	Arg	260	265	270	
Val	Pro	Val	Asn	Gln	Leu	Lys	Leu	Gly	Asp	Val	Phe	Ile	Thr	Arg	Pro	275	280	285	
Gly	Glu	Lys	Ile	Ala	Thr	Asp	Gly	Glu	Val	Asp	Glu	Gly	Ser	Ser	Ala	290	295	300	

Val Asp Glu Ser Met Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr
 305 310 315 320
 Lys Gly Ser Lys Val Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu
 325 330 335
 Met Val Lys Val Thr Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met
 340 345 350
 Ala Lys Leu Val Thr Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg
 355 360 365
 Leu Val Asp Gln Ile Ser Gln Val Phe Val Pro Val Val Ile Val Ile
 370 375 380
 Ala Ile Ala Thr Leu Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu
 385 390 395 400
 Ala Pro Ala Phe Thr Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro
 405 410 415
 Cys Ala Leu Gly Leu Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly
 420 425 430
 Arg Gly Ala Gln Leu Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu
 435 440 445
 Ser Thr Lys Lys Val Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val
 450 455 460
 Thr Thr Gly Thr Met Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser
 465 470 475 480
 Glu Thr Glu Ile Leu Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu
 485 490 495
 His Pro Ile Ala Gln Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val
 500 505 510
 Thr Asp Phe Gln Asn Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg
 515 520 525
 Gly His Glu Val Arg Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala
 530 535 540
 Leu Leu His Pro Phe Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val
 545 550 555 560
 Val Val Thr Ile Asp Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp
 565 570 575
 Thr Val Lys Asp Thr Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu
 580 585 590
 Gly Leu Thr Pro Ile Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys
 595 600 605
 Ser Val Ala Ala Glu Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu
 610 615 620
 Pro His Glu Lys Val Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys

Gly	Ala	Met	Pro	His	Ala	Thr	Gly	Gly	Arg	Leu	Asp	Gly	Arg	Val	Arg	
70					75					80					85	
gtg	gtc	ggc	cgg	gat	acg	cgt	gat	ttc	cca	cca	cgc	atg	ctt	tcc	gac	403
Val	Val	Gly	Arg	Asp	Thr	Arg	Asp	Phe	Pro	Pro	Arg	Met	Leu	Ser	Asp	
				90					95					100		
gtg	gtc	ggc	gtc	gtt	ggg	caa	gat	ccg	gcg	gca	agt	ttt	atc	acc	aac	451
Val	Val	Gly	Val	Val	Gly	Gln	Asp	Pro	Ala	Ala	Ser	Phe	Ile	Thr	Asn	
			105					110					115			
acg	gtt	gaa	gaa	gaa	ctt	gcc	tac	agc	atg	gag	caa	tta	ggg	ctc	cca	499
Thr	Val	Glu	Glu	Glu	Leu	Ala	Tyr	Ser	Met	Glu	Gln	Leu	Gly	Leu	Pro	
		120					125					130				
cct	gcg	gtc	atg	cgc	aag	cgc	gta	gag	gaa	acc	ctt	gat	ctt	tta	ggc	547
Pro	Ala	Val	Met	Arg	Lys	Arg	Val	Glu	Glu	Thr	Leu	Asp	Leu	Leu	Gly	
	135					140					145					
atc	gcg	gag	ctg	cga	tac	gtg	cca	ttg	gcg	gaa	cta	tct	ggg	ggg	gag	595
Ile	Ala	Glu	Leu	Arg	Tyr	Val	Pro	Leu	Ala	Glu	Leu	Ser	Gly	Gly	Glu	
150					155					160					165	
cag	cag	cgc	gtg	gcg	att	ggc	gcg	gtg	ctg	acc	act	cgc	ccc	gcg	ctg	643
Gln	Gln	Arg	Val	Ala	Ile	Gly	Ala	Val	Leu	Thr	Thr	Arg	Pro	Ala	Leu	
				170				175						180		
att	atc	ttg	gat	gaa	cca	acc	agc	gct	ttg	gac	cct	aat	ggg	gcc	gag	691
Ile	Ile	Leu	Asp	Glu	Pro	Thr	Ser	Ala	Leu	Asp	Pro	Asn	Gly	Ala	Glu	
			185					190					195			
gat	gtg	ctg	gca	acc	gta	acc	aag	ctg	gct	cat	gac	ttg	gcg	atg	acc	739
Asp	Val	Leu	Ala	Thr	Val	Thr	Lys	Leu	Ala	His	Asp	Leu	Ala	Met	Thr	
		200					205					210				
gta	gtg	ctt	gct	gaa	cac	cgc	atc	gag	cgc	gta	ctg	cag	tac	gtg	gac	787
Val	Val	Leu	Ala	Glu	His	Arg	Ile	Glu	Arg	Val	Leu	Gln	Tyr	Val	Asp	
		215				220					225					
cgc	gtg	gcg	cat	gtg	ggc	gct	gat	ggg	cac	gtc	act	gtt	ggg	acg	ccg	835
Arg	Val	Ala	His	Val	Gly	Ala	Asp	Gly	His	Val	Thr	Val	Gly	Thr	Pro	
230					235					240					245	
gaa	gaa	atc	atg	gct	gat	tct	gat	gtg	gca	cca	ccc	att	gtg	gaa	tta	883
Glu	Glu	Ile	Met	Ala	Asp	Ser	Asp	Val	Ala	Pro	Pro	Ile	Val	Glu	Leu	
				250					255					260		
gga	cgc	tgg	gct	ggc	tgg	gct	ccc	cta	ccg	cta	tcg	atc	cgc	gat	gca	931
Gly	Arg	Trp	Ala	Gly	Trp	Ala	Pro	Leu	Pro	Leu	Ser	Ile	Arg	Asp	Ala	
			265					270					275			
cgc	gca	cac	tcc	gct	gac	atg	cgc	aaa	cgc	ctg	tat	cag	cgt	ggg	tta	979
Arg	Ala	His	Ser	Ala	Asp	Met	Arg	Lys	Arg	Leu	Tyr	Gln	Arg	Gly	Leu	
		280					285					290				
gtg	gtg	aac	aaa	tta	cac	aac	cac	gct	gtc	cag	cca	ctt	ttg	atc	gcc	1027
Val	Val	Asn	Lys	Leu	His	Asn	His	Ala	Val	Gln	Pro	Leu	Leu	Ile	Ala	
		295				300					305					
gaa	gat	atc	atg	gtt	gat	ttc	ccc	gaa	atc	cgt	gcc	gtt	gac	ggc	gtg	1075
Glu	Asp	Ile	Met	Val	Asp	Phe	Pro	Glu	Ile	Arg	Ala	Val	Asp	Gly	Val	

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310	315							320							325			
aac ttg aat ctc	aac tcc ggt gaa att acc	gtg ctc atg ggc cga aac	1123															
Asn Leu Asn Leu	Asn Ser Gly Glu Ile Thr	Val Leu Met Gly Arg Asn																
	330	335	340															
ggc tgc gga aaa tca tcc ctg ctg tgg gct tta caa ggt tca ggg act	1171																	
Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln Gly Ser Gly Thr																		
	345	350	355															
aga aat cag ggc tcg gtg cag gtg ctt gat gag gcc gcg gga ttt tcg	1219																	
Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala Ala Gly Phe Ser																		
	360	365	370															
tgg aca gac ccc aaa act tta aag ccc gcc aag cgg cgc aat ctt gtg	1267																	
Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg Arg Asn Leu Val																		
	375	380	385															
tcc atg gtt ccg caa aca ccg acc gat att ttg tat gaa tca acc gtg	1315																	
Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr Glu Ser Thr Val																		
	390	395	400	405														
cat gca gag ctc gca cgc tct gat aaa gat gcc gca gca ccc gcc ggc	1363																	
His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala Ala Pro Ala Gly																		
	410	415	420															
acc acg cgg gaa atc ctg gat tca ctg gtc ccg aat atc ccg gac cat	1411																	
Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn Ile Pro Asp His																		
	425	430	435															
ctc cac cca cgt gat cta tca gaa ggc caa aag ctc tcc ctc gcg ctg	1459																	
Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu Ser Leu Ala Leu																		
	440	445	450															
tcc atc caa ctc gcc gca aaa ccc cgc gtg gta ttt ttc gac gaa ccc	1507																	
Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe Phe Asp Glu Pro																		
	455	460	465															
acc cgc ggc cta gac tac gac ggc aag aaa tcc ctc gcc cgc tcc ttc	1555																	
Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu Ala Arg Ser Phe																		
	470	475	480	485														
caa caa ctc gca gac gac ggc cac gcc att ttg gtg gtc acc cac gac	1603																	
Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val Val Thr His Asp																		
	490	495	500															
gtg gaa ttc tct gca ctg tgc gcc gac cga gtg ttg ttt atg gcc tct	1651																	
Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu Phe Met Ala Ser																		
	505	510	515															
gga aag atc atc tcc gat ggc aca gcc gta gaa atc ctc ccc gca tca	1699																	
Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile Leu Pro Ala Ser																		
	520	525	530															
ccg gct tac gcc cca caa gtc gca aaa atc acc gcc ggc atc caa gag	1747																	
Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala Gly Ile Gln Glu																		
	535	540	545															
gaa tca cac tgg ctc aca gtc tcg gcc gtg aaa gct gcg cta ggg cat	1795																	
Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala Ala Leu Gly His																		
	550	555	560	565														

260					265					270					
Ser	Ile	Arg	Asp	Ala	Arg	Ala	His	Ser	Ala	Asp	Met	Arg	Lys	Arg	Leu
275					280					285					
Tyr	Gln	Arg	Gly	Leu	Val	Val	Asn	Lys	Leu	His	Asn	His	Ala	Val	Gln
290					295					300					
Pro	Leu	Leu	Ile	Ala	Glu	Asp	Ile	Met	Val	Asp	Phe	Pro	Glu	Ile	Arg
305					310					315					
Ala	Val	Asp	Gly	Val	Asn	Leu	Asn	Leu	Asn	Ser	Gly	Glu	Ile	Thr	Val
325					330					335					
Leu	Met	Gly	Arg	Asn	Gly	Cys	Gly	Lys	Ser	Ser	Leu	Leu	Trp	Ala	Leu
340					345					350					
Gln	Gly	Ser	Gly	Thr	Arg	Asn	Gln	Gly	Ser	Val	Gln	Val	Leu	Asp	Glu
355					360					365					
Ala	Ala	Gly	Phe	Ser	Trp	Thr	Asp	Pro	Lys	Thr	Leu	Lys	Pro	Ala	Lys
370					375					380					
Arg	Arg	Asn	Leu	Val	Ser	Met	Val	Pro	Gln	Thr	Pro	Thr	Asp	Ile	Leu
385					390					395					
Tyr	Glu	Ser	Thr	Val	His	Ala	Glu	Leu	Ala	Arg	Ser	Asp	Lys	Asp	Ala
405					410					415					
Ala	Ala	Pro	Ala	Gly	Thr	Thr	Arg	Glu	Ile	Leu	Asp	Ser	Leu	Val	Pro
420					425					430					
Asn	Ile	Pro	Asp	His	Leu	His	Pro	Arg	Asp	Leu	Ser	Glu	Gly	Gln	Lys
435					440					445					
Leu	Ser	Leu	Ala	Leu	Ser	Ile	Gln	Leu	Ala	Ala	Lys	Pro	Arg	Val	Val
450					455					460					
Phe	Phe	Asp	Glu	Pro	Thr	Arg	Gly	Leu	Asp	Tyr	Asp	Gly	Lys	Lys	Ser
465					470					475					
Leu	Ala	Arg	Ser	Phe	Gln	Gln	Leu	Ala	Asp	Asp	Gly	His	Ala	Ile	Leu
485					490					495					
Val	Val	Thr	His	Asp	Val	Glu	Phe	Ser	Ala	Leu	Cys	Ala	Asp	Arg	Val
500					505					510					
Leu	Phe	Met	Ala	Ser	Gly	Lys	Ile	Ile	Ser	Asp	Gly	Thr	Ala	Val	Glu
515					520					525					
Ile	Leu	Pro	Ala	Ser	Pro	Ala	Tyr	Ala	Pro	Gln	Val	Ala	Lys	Ile	Thr
530					535					540					
Ala	Gly	Ile	Gln	Glu	Glu	Ser	His	Trp	Leu	Thr	Val	Ser	Ala	Val	Lys
545					550					555					
Ala	Ala	Leu	Gly	His	Gly	Glu	Ile	Ser							
565															

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<211> 1343

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1320)

<223> FRXA00702

<400> 105

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gat ctt tta ggc atc gcg gag ctg cga tac gtg cca ttg gcg gaa cta	96
Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu	
20 25 30	
tct ggt ggt gag cag cag cgc gtg gcg att ggc gcg gtg ctg acc act	144
Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr	
35 40 45	
cgc ccc gcg ctg att atc ttg gat gaa cca acc agc gct ttg gac cct	192
Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro	
50 55 60	
aat ggt gcc gag gat gtg ctg gca acc gta acc aag ctg gct cat gac	240
Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp	
65 70 75 80	
ttg gcg atg acc gta gtg ctt gct gaa cac cgc atc gag cgc gta ctg	288
Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu	
85 90 95	
cag tac gtg gac cgc gtg gcg cat gtg ggc gct gat ggg cac gtc act	336
Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val Thr	
100 105 110	
gtt ggg acg ccg gaa gaa atc atg gct gat tct gat gtg gca cca ccc	384
Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro	
115 120 125	
att gtg gaa tta gga cgc tgg gct ggc tgg gct ccc cta ccg cta tcg	432
Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser	
130 135 140	
atc cgc gat gca cgc gca cac tcc gct gac atg cgc aaa cgc ctg tat	480
Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr	
145 150 155 160	
cag cgt ggt tta gtg gtg aac aaa tta cac aac cac gct gtc cag cca	528
Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln Pro	
165 170 175	
ctt ttg atc gcc gaa gat atc atg gtt gat ttc ccc gaa atc cgt gcc	576
Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala	
180 185 190	
gtt gac gcc gtg aac ttg aat ctc aac tcc ggt gaa att acc gtg ctc	624
Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu	
195 200 205	

<210> 106

<211> 440

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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Asp	Leu	Leu	Gly	Ile	Ala	Glu	Leu	Arg	Tyr	Val	Pro	Leu	Ala	Glu	Leu
			20					25					30		

Ser	Gly	Gly	Glu	Gln	Gln	Arg	Val	Ala	Ile	Gly	Ala	Val	Leu	Thr	Thr
		35					40					45			

Arg	Pro	Ala	Leu	Ile	Ile	Leu	Asp	Glu	Pro	Thr	Ser	Ala	Leu	Asp	Pro
	50					55					60				

Asn	Gly	Ala	Glu	Asp	Val	Leu	Ala	Thr	Val	Thr	Lys	Leu	Ala	His	Asp
65					70					75					80

Leu	Ala	Met	Thr	Val	Val	Leu	Ala	Glu	His	Arg	Ile	Glu	Arg	Val	Leu
				85						90				95	

Gln	Tyr	Val	Asp	Arg	Val	Ala	His	Val	Gly	Ala	Asp	Gly	His	Val	Thr
			100					105					110		

Val	Gly	Thr	Pro	Glu	Glu	Ile	Met	Ala	Asp	Ser	Asp	Val	Ala	Pro	Pro
		115					120					125			

Ile	Val	Glu	Leu	Gly	Arg	Trp	Ala	Gly	Trp	Ala	Pro	Leu	Pro	Leu	Ser
130						135					140				

Ile	Arg	Asp	Ala	Arg	Ala	His	Ser	Ala	Asp	Met	Arg	Lys	Arg	Leu	Tyr
145					150					155					160

Gln	Arg	Gly	Leu	Val	Val	Asn	Lys	Leu	His	Asn	His	Ala	Val	Gln	Pro
			165						170					175	

Leu	Leu	Ile	Ala	Glu	Asp	Ile	Met	Val	Asp	Phe	Pro	Glu	Ile	Arg	Ala
			180					185					190		

Val	Asp	Gly	Val	Asn	Leu	Asn	Leu	Asn	Ser	Gly	Glu	Ile	Thr	Val	Leu
		195					200					205			

Met	Gly	Arg	Asn	Gly	Cys	Gly	Lys	Ser	Ser	Leu	Leu	Trp	Ala	Leu	Gln
	210					215					220				

Gly	Ser	Gly	Thr	Arg	Asn	Gln	Gly	Ser	Val	Gln	Val	Leu	Asp	Glu	Ala
225					230					235					240

Ala	Gly	Phe	Ser	Trp	Thr	Asp	Pro	Lys	Thr	Leu	Lys	Pro	Ala	Lys	Arg
				245					250					255	

Arg	Asn	Leu	Val	Ser	Met	Val	Pro	Gln	Thr	Pro	Thr	Asp	Ile	Leu	Tyr
			260					265						270	

Glu	Ser	Thr	Val	His	Ala	Glu	Leu	Ala	Arg	Ser	Asp	Lys	Asp	Ala	Ala
		275					280					285			

Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn
 290 295 300

Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu
 305 310 315 320

Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe
 325 330 335

Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu
 340 345 350

Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val
 355 360 365

Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu
 370 375 380

Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile
 385 390 395 400

Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala
 405 410 415

Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala
 420 425 430

Ala Leu Gly His Gly Glu Ile Ser
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<210> 107

<211> 576

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(553)

<223> RXN00828

<400> 107

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tgcttccgcg aaaagtgggc agctggaact ctctgacacg gtg cgc ggc ggc ctt 115
 Val Arg Gly Gly Leu
 1 5

aac acg ccc ccg cac aag tgg cgt tca gct gat cta gct gca cgt att 163
 Asn Thr Pro Pro His Lys Trp Arg Ser Ala Asp Leu Ala Ala Arg Ile
 10 15 20

ggc act gtc ttt cag gat cca gag cac caa ttt gtg gcg cgc act gtg 211
 Gly Thr Val Phe Gln Asp Pro Glu His Gln Phe Val Ala Arg Thr Val
 25 30 35

cgt gat gag cta gaa att ggg ccg aaa atc atg aaa gtc gat gca agc 259
 Arg Asp Glu Leu Glu Ile Gly Pro Lys Ile Met Lys Val Asp Ala Ser
 40 45 50

gag cgc atc gag gag ctg ctt gat cgt ttg cgc ctc cgc cac ttg gaa 307

Glu Arg Ile Glu Glu Leu Leu Asp Arg Leu Arg Leu Arg His Leu Glu
 55 60 65
 aac gcc aat ccg ttt acc ttg agt ggt gga gaa aag cgc cgc cta tct 355
 Asn Ala Asn Pro Phe Thr Leu Ser Gly Gly Glu Lys Arg Arg Leu Ser
 70 75 80 85
 gtg gcg aca gcc ttg gtg gca gca ccg aaa ctt ctc att ttg gat gag 403
 Val Ala Thr Ala Leu Val Ala Ala Pro Lys Leu Leu Ile Leu Asp Glu
 90 95 100
 cct acg ttt ggc caa gat ccc gag acc ttc aca gag ctg gtg acc atg 451
 Pro Thr Phe Gly Gln Asp Pro Glu Thr Phe Thr Glu Leu Val Thr Met
 105 110 115
 ttg cgt gaa tta aca gac aac gga atc agc att gtg tcg gta acc cat 499
 Leu Arg Glu Leu Thr Asp Asn Gly Ile Ser Ile Val Ser Val Thr His
 120 125 130
 gat cct gat ttc atc gca gcg ctg ggc gat cac cac att gag gtg agc 547
 Asp Pro Asp Phe Ile Ala Ala Leu Gly Asp His His Ile Glu Val Ser
 135 140 145
 gcg aag tgaacctgct gatcaaaatt aat 576
 Ala Lys
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 <213> Corynebacterium glutamicum
 <400> 108
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 20 25 30
 Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly Pro Lys Ile Met
 35 40 45
 Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu Asp Arg Leu Arg
 50 55 60
 Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu Ser Gly Gly Glu
 65 70 75 80
 Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala Ala Pro Lys Leu
 85 90 95
 Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro Glu Thr Phe Thr
 100 105 110
 Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn Gly Ile Ser Ile
 115 120 125
 Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala Leu Gly Asp His
 130 135 140

GENE 300 - PHEU-500

His Ile Glu Val Ser Ala Lys
145 150

<210> 109
<211> 392
<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (1)..(369)
<223> FRXA00828

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ccg aaa atc atg aaa gtt gat gca agc gag cgc atc gag gag ttg ctt 96
Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu
20 25 30
gat cgg ttg cgc ctc cgc cac tta gaa aat gct aat ccg ttt acc ttg 144
Asp Arg Leu Arg Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu
35 40 45
agt ggt gga gaa aag cgc cgc cta tct gtg gcg aca gcc ttg gtg gca 192
Ser Gly Gly Glu Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala
50 55 60
gca ccg aaa ctt ctc att ttg gat gag cct acg ttt ggc caa gat ccc 240
Ala Pro Lys Leu Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro
65 70 75 80
gag acc ttc aca gag ctg gtg acg atg ttg cgt gaa tta aca gac aac 288
Glu Thr Phe Thr Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn
85 90 95
gga atc agc att gtg tca gta acc cat gat cct gat ttc atc gca gcg 336
Gly Ile Ser Ile Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala
100 105 110
ctg ggc gat cac cac att gag gtg agc gcg aag tgaacctgct gatcaaaatt 389
Leu Gly Asp His His Ile Glu Val Ser Ala Lys
115 120
aat 392

<210> 110
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<213> *Corynebacterium glutamicum*

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Glu His Gln Phe Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly
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Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu
20 25 30

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 Asp Gln Leu Leu Leu Ile Pro Arg Leu Gly Arg Ile Leu Pro Pro Ser
 105 110 115

cgc agc gca cgc acc caa cac aaa gac aaa gcc ctt tca ctt ctg aac 499
 Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala Leu Ser Leu Leu Asn
 120 125 130

tcc atc gga ctc ggc gac tta gca aaa cgc aag gtc agc gaa cta tcc 547
 Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys Val Ser Glu Leu Ser
 135 140 145

ggt gga caa caa gcc cgc gtt aac ttg gcc cgc gcg ctg atg aac tcc 595
 Gly Gly Gln Gln Ala Arg Val Asn Leu Ala Arg Ala Leu Met Asn Ser
 150 155 160 165

ccc aag ctc ctg ctt gtc gat gaa ccc acc gcc gcc ctc gat caa cat 643
 Pro Lys Leu Leu Leu Val Asp Glu Pro Thr Ala Ala Leu Asp Gln His
 170 175 180

tcc gcc agc gaa gtc acc gaa cta atc gtc tcg atg gcc cac caa tac 691
 Ser Ala Ser Glu Val Thr Glu Leu Ile Val Ser Met Ala His Gln Tyr
 185 190 195

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 Asn Ala Pro Thr
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<210> 112

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

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 1 5 10 15

Thr Ser Arg Thr Leu Leu Asn Asn Ile His Phe Trp Met Ser Asn Gln
 20 25 30

Ala Lys Ser Ser Val Ser Pro Ala His Pro Ala Pro Glu Asn Pro Pro
 35 40 45

Tyr Ser Pro Ser Ser Ala Ala Ser Lys Ala Pro Asp Ser Gly Thr Ala
 50 55 60

Thr Leu Gly Asp Ile Asp Leu Leu Asn Pro Gln Asn Arg Ala Ala Leu
 65 70 75 80

Arg Arg Asn His Leu Gly Ile Val Phe Gln Gln Pro Asn Leu Leu Pro
 85 90 95

Ser Leu Thr Val Leu Asp Gln Leu Leu Leu Ile Pro Arg Leu Gly Arg
 100 105 110

Ile Leu Pro Pro Ser Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala
 115 120 125

Leu Ser Leu Leu Asn Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys
 130 135 140

acc atg ctt gtt gtc acc cac gaa atg ggc ttc gcc cac gaa gtc gcc 480
 Thr Met Leu Val Val Thr His Glu Met Gly Phe Ala His Glu Val Ala
 145 150 155 160

gac cag gtc gtg ttc atg gcc gat gga gtt gtc gtt gaa gcc gga acc 528
 Asp Gln Val Val Phe Met Ala Asp Gly Val Val Val Glu Ala Gly Thr
 165 170 175

ccc gaa caa gtt ctg gac aat cca aag gaa cag cgc acc aaa gac ttc 576
 Pro Glu Gln Val Leu Asp Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe
 180 185 190

ctg tct tct ctg ctc taaccttttc gggtcttaaa aaa 614
 Leu Ser Ser Leu Leu
 195

<210> 114

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

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Arg Asp Gly Val Leu Tyr Glu Ile Ser Glu Lys Asp Ala Ala Lys Gln
 20 25 30

Arg Ser Asp Ile Gly Met Val Phe Gln Asn Phe Asn Leu Phe Pro His
 35 40 45

Arg Thr Val Ile Glu Asn Ile Ile Glu Ala Pro Ile His Val Lys Lys
 50 55 60

Gln Pro Glu Ser Lys Ala Arg Ala Arg Ala Met Glu Leu Leu Glu Gln
 65 70 75 80

Val Gly Leu Ala His Lys Ala Asp Ala Tyr Pro Val Gln Leu Ser Gly
 85 90 95

Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Ala Met Glu Pro
 100 105 110

Lys Leu Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu
 115 120 125

Val Gly Glu Val Leu Arg Val Met Lys Gln Leu Ala Asp Asp Gly Met
 130 135 140

Thr Met Leu Val Val Thr His Glu Met Gly Phe Ala His Glu Val Ala
 145 150 155 160

Asp Gln Val Val Phe Met Ala Asp Gly Val Val Val Glu Ala Gly Thr
 165 170 175

Pro Glu Gln Val Leu Asp Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe
 180 185 190

Leu Ser Ser Leu Leu
 195

<210> 115
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(742)
 <223> RXN02570

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cattggttcc gcagcgggtt ccggaggacg tcgcttaaac atg aat cct ttg aca 115
                                         Met Asn Pro Leu Thr
                                         1 5

tgg atc att ggc gca ttc agc atg tgg atc gtg gtg ctg ggc gtt aat 163
Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val Val Leu Gly Val Asn
                        10 15 20

aag ctt ggt tta agc atc gca gtg atc atc atc gcg cag gtc gtg gcg 211
Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile Ala Gln Val Val Ala
                        25 30 35

atg att cgg gtg cgc aat gta tct gtg ttg gct tca aca gca ttg tta 259
Met Ile Arg Val Arg Asn Val Ser Val Leu Ala Ser Thr Ala Leu Leu
                        40 45 50

tcg gtt cct gca ttg gcc tcg atg gcg ctg att cac atg ccg tat tct 307
Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile His Met Pro Tyr Ser
                        55 60 65

tcc gac ggc tgg ttg att gct ctt acc ttg acg gct cgt ttt agt gcg 355
Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr Ala Arg Phe Ser Ala
                        70 75 80 85

ttg atg tct att ttc ctc ctt gca gca aca gcg att act att cct gag 403
Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala Ile Thr Ile Pro Glu
                        90 95 100

ctg gtg aaa tcc cta tat cgt tgg ccc aag ctg gcg tat atc gtg ggt 451
Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu Ala Tyr Ile Val Gly
                        105 110 115

tct gca ttg cag atg att ccg cag ggt aaa cag acc ttg gcg ttg gtt 499
Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln Thr Leu Ala Leu Val
                        120 125 130

cgt gat gcc aat gct ttg cgc ggg cgc agc gtt aaa ggt ccc gtg cgc 547
Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val Lys Gly Pro Val Arg
                        135 140 145

gcg gtg aaa tat gtg ggt ttg ccc ctg att aca cat tta ctt agt gca 595
Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr His Leu Leu Ser Ala
                        150 155 160 165

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<210> 116
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Met Thr Lys Arg Thr 1 5															
aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg 163															
Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp 10 15 20															
gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc 211															
Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser 25 30 35															
aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat 259															
Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp 40 45 50															
aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca 307															
Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala 55 60 65															
gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct 355															
Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Thr Ala Ile Ala 70 75 80 85															
gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc 403															
Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe 90 95 100															
ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc 451															
Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe 105 110 115															
ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc 499															
Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu 120 125 130															
aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc 547															
Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe 135 140 145															
gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg 595															
Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu 150 155 160 165															
ccc tgg gaa ctc gaa gaa tca qca cgt gtc gac ggc gcc aca cgt gcc 643															

Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly
170 175 180

caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt 691
Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe
185 190 195

acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg 739
Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu
200 205 210

gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc 787
Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile
215 220 225

gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc 835
Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val
230 235 240 245

atg gca gcg gga gct ttg gtg acc atc cca ctg atc atc atg gtt ctc 883
Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu Ile Ile Met Val Leu
250 255 260

atc ttc caa cgc cgc atc gtc tcc gga ctc acc gca ggt ggc gtg aaa 931
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265 270 275

gcc tagactagat actcatgagt gct 957
Ala

<210> 118
<211> 278
<212> PRT
<213> Corynebacterium glutamicum

<400> 118
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Ala Leu Arg Asp Ser Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr
35 40 45

His Val Thr Leu Asp Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly
50 55 60

Asn Asn Phe Leu Ala Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr
65 70 75 80

Thr Thr Ala Ile Ala Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu
85 90 95

Ala Arg Leu Glu Phe Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu
100 105 110

Ala Ala Ser Met Phe Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln
115 120 125

Leu Phe Gly Asp Leu Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile
 130 135 140
 Pro Asn Ile Ser Phe Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser
 145 150 155 160
 Phe Phe Arg Gln Leu Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp
 165 170 175
 Gly Ala Thr Arg Gly Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala
 180 185 190
 Ala Pro Ala Leu Phe Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp
 195 200 205
 Asn Glu Phe Met Leu Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro
 210 215 220
 Val Thr Val Ala Ile Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr
 225 230 235 240
 Pro Tyr Ala Ser Val Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu
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 Ile Ile Met Val Leu Ile Phe Gln Arg Arg Ile Val Ser Gly Leu Thr
 260 265 270
 Ala Gly Gly Val Lys Ala
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 <212> DNA
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 <222> (101)..(889)
 <223> FRXA02354

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 Met Thr Lys Arg Thr
 1 5

aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg 163
 Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp
 10 15 20

gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc 211
 Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser
 25 30 35

aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat 259
 Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp
 40 45 50

aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca 307
 Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala
 55 60 65
 gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct 355
 Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Thr Ala Ile Ala
 70 75 80 85
 gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc 403
 Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe
 90 95 100
 ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc 451
 Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe
 105 110 115
 ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc 499
 Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu
 120 125 130
 aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc 547
 Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe
 135 140 145
 gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg 595
 Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu
 150 155 160 165
 ccc tgg gaa ctc gaa gaa tca gca cgt gtc gac ggc gcc aca cgt ggc 643
 Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly
 170 175 180
 caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt 691
 Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe
 185 190 195
 acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg 739
 Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu
 200 205 210
 gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc 787
 Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile
 215 220 225
 gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc 835
 Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val
 230 235 240 245
 atg gca gcg gga gct ttg gtg acc atc cca ctg atc atc atg gtt ctc 883
 Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu Ile Ile Met Val Leu
 250 255 260
 atc ttc 889
 Ile Phe

<210> 120

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Met Thr Lys Arg Thr Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val
 1 5 10 15

Phe Ile Leu Phe Trp Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr
 20 25 30

Ala Leu Arg Asp Ser Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr
 35 40 45

His Val Thr Leu Asp Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly
 50 55 60

Asn Asn Phe Leu Ala Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr
 65 70 75 80

Thr Thr Ala Ile Ala Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu
 85 90 95

Ala Arg Leu Glu Phe Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu
 100 105 110

Ala Ala Ser Met Phe Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln
 115 120 125

Leu Phe Gly Asp Leu Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile
 130 135 140

Pro Asn Ile Ser Phe Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser
 145 150 155 160

Phe Phe Arg Gln Leu Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp
 165 170 175

Gly Ala Thr Arg Gly Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala
 180 185 190

Ala Pro Ala Leu Phe Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp
 195 200 205

Asn Glu Phe Met Leu Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro
 210 215 220

Val Thr Val Ala Ile Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr
 225 230 235 240

Pro Tyr Ala Ser Val Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu
 245 250 255

Ile Ile Met Val Leu Ile Phe
 260

<210> 121

<211> 1251

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<223> RXN00001

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ttc aaa gat gct tcc cta agc tac ccg gga gca aag gaa ccc acc gtc 163
Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala Lys Glu Pro Thr Val
10 15 20

aag aaa ttc aac ctg gaa atc gcc gat ggc gag ttc ctc gtc ctc gtc 211
Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
25 30 35

ggc cct tcc ggc tgt ggt aaa tcc acc acg ctg cgc atg ctg gcc ggt 259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Met Leu Ala Gly
40 45 50

ttg gaa aac gtt act gac ggt gcc att ttc atc gga gac aag gac gtt 307
Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile Gly Asp Lys Asp Val
55 60 65

acc cac gtt gca ccg cgt gac cgt gac atc gcc atg gtt ttc cag aac 355
Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala Met Val Phe Gln Asn
70 75 80 85

tat	gct	ctc	tac	ccc	cac	atg	acc	gtg	ggc	gag	aac	atg	ggc	ttc	gca	403
Tyr	Ala	Leu	Tyr	Pro	His	Met	Thr	Val	Gly	Glu	Asn	Met	Gly	Phe	Ala	
				90					95					100		

ctg aag atc gcc ggc aag tcc caa gac gag atc aat aag cgc gtc gac 451
Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile Asn Lys Arg Val Asp
105 110 115

gaa gcc gcc gcc act ttg ggc ctg acc gaa ttc ttg gag cgc aag ccg 499
Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe Leu Glu Arg Lys Pro
120 125 130

aag gcc ctg tcc ggt ggt cag cgt cag cgt gtg gcc atg ggc cgc gcc 547
Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
135 140 145

att gtt cgc aac ccg cag gtc ttt ctc atg gat gag ccg ctg tct aac 595
Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp Glu Pro Leu Ser Asn
150 155 160 165

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ctc gat gcc aag ctg cgt gtt cag acc cgt acc cag att gca gcc ctg      643
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr Gln Ile Ala Ala Leu
          170                      175                      180

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cag cgc aag ctt ggg gtt acc acc gtt tac gtc acc cac gac cag acg 691
Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Thr
185 190 195

gag gcc ttg acc atg ggt gac cgc atc gcg gtg ctg aag gat ggc tac 739
Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val Leu Lys Asp Gly Tyr
200 205 210

ctg cag cag gtt ggc gcg ccc cga gag ctt tat gac cgc ccc gcc aac 787
 Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr Asp Arg Pro Ala Asn
 215 220 225

gtc ttc gtc gcc ggc ttc atc ggc tcc cca gcc atg aac ttg ggc acc 835
 Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala Met Asn Leu Gly Thr
 230 235 240 245

ttc tcg gtc aag gat ggt gac gct acc tct ggt cac gct cgc atc aag 883
 Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly His Ala Arg Ile Lys
 250 255 260

ctt tcc ccg gaa acc ctc gcc gcc atg acg ccg gag gat aat ggc cgc 931
 Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro Glu Asp Asn Gly Arg
 265 270 275

atc acc att ggt ttc cgc ccg gag gca ctg gag atc att ccg gaa ggc 979
 Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu Ile Ile Pro Glu Gly
 280 285 290

gag tcc acc gat ctt tcc atc cca atc aag ctc gac ttc gtg gag gaa 1027
 Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu Asp Phe Val Glu Glu
 295 300 305

ctc ggt tcc gat tcc ttc ctc tac ggc aag ctg gta ggc gag ggc gac 1075
 Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu Val Gly Glu Gly Asp
 310 315 320 325

ctt gga tcc tcc agc gag gat gtc ccc gag tcc ggc caa atc gtc gtc 1123
 Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser Gly Gln Ile Val Val
 330 335 340

cgc gct gct ccg aac gcc gcg cct gct ccg ggc agt gtt ttc cac gca 1171
 Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly Ser Val Phe His Ala
 345 350 355

cgc atc gtg gag ggc ggc cag cac aac ttc tcg gcg tcg act ggc aag 1219
 Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser Ala Ser Thr Gly Lys
 360 365 370

cgc ctc cct taagcccgcg taccggctac ccc 1251
 Arg Leu Pro
 375

<210> 122

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Met Ala Thr Val Thr Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala
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Lys Glu Pro Thr Val Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu
 20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
 35 40 45

Arg Met Leu Ala Gly Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile
 50 55 60
 Gly Asp Lys Asp Val Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala
 65 70 75 80
 Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu
 85 90 95
 Asn Met Gly Phe Ala Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile
 100 105 110
 Asn Lys Arg Val Asp Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe
 115 120 125
 Leu Glu Arg Lys Pro Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
 130 135 140
 Ala Met Gly Arg Ala Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp
 145 150 155 160
 Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr
 165 170 175
 Gln Ile Ala Ala Leu Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val
 180 185 190
 Thr His Asp Gln Thr Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val
 195 200 205
 Leu Lys Asp Gly Tyr Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr
 210 215 220
 Asp Arg Pro Ala Asn Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala
 225 230 235 240
 Met Asn Leu Gly Thr Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly
 245 250 255
 His Ala Arg Ile Lys Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro
 260 265 270
 Glu Asp Asn Gly Arg Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu
 275 280 285
 Ile Ile Pro Glu Gly Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu
 290 295 300
 Asp Phe Val Glu Glu Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu
 305 310 315 320
 Val Gly Glu Gly Asp Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser
 325 330 335
 Gly Gln Ile Val Val Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly
 340 345 350
 Ser Val Phe His Ala Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser
 355 360 365
 Ala Ser Thr Gly Lys Arg Leu Pro

002299-446660

370

375

<210> 123
 <211> 1251
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1228)
 <223> FRXA00001

<400> 123

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gatcgttcgg cacgtacctg ccgatggagg agattctgca atg gca acc gta acg 115
 Met Ala Thr Val Thr
 1 5

ttc aaa gat gct tcc cta agc tac ccg gga gca aag gaa ccc acc gtc 163
 Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala Lys Glu Pro Thr Val
 10 15 20

aag aaa ttc aac ctg gaa atc gcc gat ggc gag ttc ctc gtc ctc gtc 211
 Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
 25 30 35

ggc cct tcc ggc tgt ggt aaa tcc acc acg ctg cgc atg ctg gcc ggt 259
 Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Met Leu Ala Gly
 40 45 50

ttg gaa aac gtt act gac ggt gcc att ttc atc gga gac aag gac gtt 307
 Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile Gly Asp Lys Asp Val
 55 60 65

acc cac gtt gca ccg cgt gac cgt gac atc gcc atg gtt ttc cag aac 355
 Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala Met Val Phe Gln Asn
 70 75 80 85

tat gct ctc tac ccc cac atg acc gtg ggc gag aac atg ggc ttc gca 403
 Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu Asn Met Gly Phe Ala
 90 95 100

ctg aag atc gcc ggc aag tcc caa gac gag atc aat aag cgc gtc gac 451
 Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile Asn Lys Arg Val Asp
 105 110 115

gaa gcc gcc gcc act ttg ggc ctg acc gaa ttc ttg gag cgc aag ccg 499
 Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe Leu Glu Arg Lys Pro
 120 125 130

aag gcc ctg tcc ggt ggt cag cgt cag cgt gtg gcc atg ggc cgc gcc 547
 Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
 135 140 145

att gtt cgc aac ccg cag gtc ttt ctc atg gat gag ccg ctg tct aac 595
 Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp Glu Pro Leu Ser Asn
 150 155 160 165

ctc gat gcc aag ctg cgt gtt cag acc cgt acc cag att gca gcc ctg 643

Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr Gln Ile Ala Ala Leu
 170 175 180
 cag cgc aag ctt ggg gtt acc acc gtt tac gtc acc cac gac cag acg 691
 Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Thr
 185 190 195
 gag gcc ttg acc atg ggt gac cgc atc gcg gtg ctg aag gat ggc tac 739
 Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val Leu Lys Asp Gly Tyr
 200 205 210
 ctg cag cag gtt ggc gcg ccc cga gag ctt tat gac cgc ccc gcc aac 787
 Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr Asp Arg Pro Ala Asn
 215 220 225
 gtc ttc gtc gcc ggc ttc atc ggc tcc cca gcc atg aac ttg ggc acc 835
 Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala Met Asn Leu Gly Thr
 230 235 240 245
 ttc tcg gtc aag gat ggt gac gct acc tct ggt cac gct cgc atc aag 883
 Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly His Ala Arg Ile Lys
 250 255 260
 ctt tcc ccg gaa acc ctc gcc gcc atg acg ccg gag gat aat ggc cgc 931
 Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro Glu Asp Asn Gly Arg
 265 270 275
 atc acc att ggt ttc cgc ccg gag gca ctg gag atc att ccg gaa ggc 979
 Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu Ile Ile Pro Glu Gly
 280 285 290
 gag tcc acc gat ctt tcc atc cca atc aag ctc gac ttc gtg gag gaa 1027
 Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu Asp Phe Val Glu Glu
 295 300 305
 ctc ggt tcc gat tcc ttc ctc tac ggc aag ctg gta ggc gag ggc gac 1075
 Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu Val Gly Glu Gly Asp
 310 315 320 325
 ctt gga tcc tcc agc gag gat gtc ccc gag tcc ggc caa atc gtc gtc 1123
 Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser Gly Gln Ile Val Val
 330 335 340
 cgc gct gct ccg aac gcc gcg cct gct ccg ggc agt gtt ttc cac gca 1171
 Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly Ser Val Phe His Ala
 345 350 355
 cgc atc gtg gag ggc ggc cag cac aac ttc tcg gcg tcg act ggc aag 1219
 Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser Ala Ser Thr Gly Lys
 360 365 370
 cgc ctc cct taagcccgcg taccggctac ccc 1251
 Arg Leu Pro
 375

<210> 124

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

Met Ala Thr Val Thr Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala
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Lys Glu Pro Thr Val Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu
20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
35 40 45

Arg Met Leu Ala Gly Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile
50 55 60

Gly Asp Lys Asp Val Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala
65 70 75 80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu
85 90 95

Asn Met Gly Phe Ala Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile
100 105 110

Asn Lys Arg Val Asp Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe
115 120 125

Leu Glu Arg Lys Pro Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
130 135 140

Ala Met Gly Arg Ala Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp
145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr
165 170 175

Gln Ile Ala Ala Leu Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val
180 185 190

Thr His Asp Gln Thr Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val
195 200 205

Leu Lys Asp Gly Tyr Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr
210 215 220

Asp Arg Pro Ala Asn Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala
225 230 235 240

Met Asn Leu Gly Thr Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly
245 250 255

His Ala Arg Ile Lys Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro
260 265 270

Glu Asp Asn Gly Arg Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu
275 280 285

Ile Ile Pro Glu Gly Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu
290 295 300

Asp Phe Val Glu Glu Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu
305 310 315 320

aag gat tta tcg ggt ggt cag cgt cag cgt gtg gcg atg ggt cgc gcg 547
Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
135 140 145

ttg gtg cgt gat ccg aag gtg ttc ctc atg gat gag ccg ctg tcc aac 595
Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp Glu Pro Leu Ser Asn
150 155 160 165

ctg gat gcg aaa ttg cgc gtg caa acc cgc gcg gag gtc gct gct ttg 643
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala Glu Val Ala Ala Leu
170 175 180

cag cgt cgc ctg ggc acc acc acg gtg tat gtc acc cac gat cag gtt 691
Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val Thr His Asp Gln Val
185 190 195

gag gca atg acg atg ggc gat cgg gtt gcg gtg ctc aag gac ggg ttg 739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Lys Asp Gly Leu
200 205 210

ctg cag cag gtc gca ccg ccc agg gag ctt tac gac gcc ccg gtc aac 787
Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr Asp Ala Pro Val Asn
215 220 225

gaa ttc gtt gcg ggc ttc atc ggc tcg ccg tcc atg aac ctc ttc cct 835
Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser Met Asn Leu Phe Pro
230 235 240 245

gcc aac ggg cac aag atg ggt gtg cgc ccg gag aag atg ctg gtc aat 883
Ala Asn Gly His Lys Met Gly Val Arg Pro Glu Lys Met Leu Val Asn
250 255 260

gag acc cct gag ggt ttc aca agc att gat gct gtg gtg gat atc gtc 931
Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala Val Val Asp Ile Val
265 270 275

gag gag ctt ggc tcc gaa tcg tat gtt tat gcc act tgg gag ggc cac 979
Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala Thr Trp Glu Gly His
280 285 290

cgc ctg gtg gcc cgt tgg gtg gaa ggc ccc gtg cca gcc cct ggc acg 1027
Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val Pro Ala Pro Gly Thr
295 300 305

cct gtg act ttt tcc tat gat gcg gcg cag gcg cat cat ttc gat ctg 1075
Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala His His Phe Asp Leu
310 315 320 325

gag tcg ggc gag cgt atc gct tagtttcgga cgtggggagg cgt 1119
Glu Ser Gly Glu Arg Ile Ala
330

<210> 126

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

Met Ala Thr Val Thr Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala

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Glu Arg Ala Thr Val His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu	20	25	30
Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu	35	40	45
Arg Ala Leu Ala Gly Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile	50	55	60
Asp Gly Lys Asp Val Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala	65	70	75
Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys	85	90	95
Asn Met Gly Phe Ala Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile	100	105	110
Asp Ala Lys Val Asn Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe	115	120	125
Leu Asp Arg Lys Pro Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val	130	135	140
Ala Met Gly Arg Ala Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp	145	150	155
Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala	165	170	175
Glu Val Ala Ala Leu Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val	180	185	190
Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val	195	200	205
Leu Lys Asp Gly Leu Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr	210	215	220
Asp Ala Pro Val Asn Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser	225	230	235
Met Asn Leu Phe Pro Ala Asn Gly His Lys Met Gly Val Arg Pro Glu	245	250	255
Lys Met Leu Val Asn Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala	260	265	270
Val Val Asp Ile Val Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala	275	280	285
Thr Trp Glu Gly His Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val	290	295	300
Pro Ala Pro Gly Thr Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala	305	310	315
His His Phe Asp Leu Glu Ser Gly Glu Arg Ile Ala	325	330	

<210> 127
 <211> 1369
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1369)
 <223> RXN02455

<400> 127

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gctcatcacc ccgcttttta tcaagaaaga tgaggacctc ttg aag cgt ctt act 115
                                   Leu Lys Arg Leu Thr
                                   1      5

cgc atc gca tcc atc agc atg gcc tcc atg ctc gcc gcc gca agt ctc 163
Arg Ile Ala Ser Ile Ser Met Ala Ser Met Leu Ala Ala Ala Ser Leu
                                   10      15      20

gtc gcg tgc tcc ggc tcc acc gac gag gaa ggc gat gtt tac ttc ctg 211
Val Ala Cys Ser Gly Ser Thr Asp Glu Gly Asp Val Tyr Phe Leu
                                   25      30      35

aac ttc aag cct gaa cag gac gtg gca tac cag gaa atc gca aag gcc 259
Asn Phe Lys Pro Glu Gln Asp Val Ala Tyr Gln Glu Ile Ala Lys Ala
                                   40      45      50

tac act gaa gag acc ggc gtt aag gtc aag gtc gtt act gcc gcc tcc 307
Tyr Thr Glu Glu Thr Gly Val Lys Val Lys Val Val Thr Ala Ala Ser
                                   55      60      65

ggc tcc tat gag cag acc ctc aag gcc gag att ggc aag gac gaa gcc 355
Gly Ser Tyr Glu Gln Thr Leu Lys Ala Glu Ile Gly Lys Asp Glu Ala
                                   70      75      80      85

ccg act ctc ttc cag gtc aat ggc cca gcc ggc ttc atc act tgg cag 403
Pro Thr Leu Phe Gln Val Asn Gly Pro Ala Gly Phe Ile Thr Trp Gln
                                   90      95      100

gac tac atg gca gat atg tcg gac acc gag gta gct aag cag ctg acc 451
Asp Tyr Met Ala Asp Met Ser Asp Thr Glu Val Ala Lys Gln Leu Thr
                                   105      110      115

gac gac att ccg ccg ctg acc acc gag gat ggc gag gta cgt ggc gtt 499
Asp Asp Ile Pro Pro Leu Thr Thr Glu Asp Gly Glu Val Arg Gly Val
                                   120      125      130

ccg ttc gcc gtc gag ggc ttc ggc atc atc tac aac gac gag atc ttc 547
Pro Phe Ala Val Glu Gly Phe Gly Ile Ile Tyr Asn Asp Glu Ile Phe
                                   135      140      145

gac aag tac atc gcc acg tcc ggc gca aag atc aag tcc acg gat gag 595
Asp Lys Tyr Ile Ala Ser Ser Gly Ala Lys Ile Lys Ser Thr Asp Glu
                                   150      155      160      165

atc acg agc tac cag aag ctc aag gaa gtc gcc gag gat atg cag gca 643
Ile Thr Ser Tyr Gln Lys Leu Lys Glu Val Ala Glu Asp Met Gln Ala

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260	265	270
Ala Met Val Gln Asn Gly Asn Trp	Ala Trp Ser Gln Ile Ser Glu Thr	
275	280	285
Ser Gly Asn Val Val Lys Glu Asp Lys Ile Lys Phe Leu Pro Met Tyr		
290	295	300
Met Gly Leu Pro Asp Glu Glu Lys His Gly Ile Asn Val Gly Thr Glu		
305	310	315
Asn Tyr Leu Gly Val Asn Ser Glu Ala Ser Glu Val Asp Gln Gln Ala		
325	330	335
Thr Lys Asp Phe Val Asp Trp Leu Phe Thr Ser Glu Ala Gly Lys Glu		
340	345	350
His Val Val Lys Asp Leu Gly Phe Ile Ala Pro Phe Glu Ser Tyr Thr		
355	360	365
Ala Glu Asn Thr Pro Asn Asp Pro Leu Ser Glu Gln Val Ala Glu Ala		
370	375	380
Ile Ala Asn Lys Asp Leu Thr Thr Tyr Pro Trp Asn Phe Gln Tyr Phe		
385	390	395
Pro Ser Gln Gln Phe Lys Asp Asp Phe Gly Gln Asp Leu Ser Gln Tyr		
405	410	415
Ala Ser Gly Lys Leu Lys Trp		
420		

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 <223> RXN02795

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 Val Leu Lys Val Ser 5
 gat tta acg gtt ggc aac aat ttt gtc cac aac gtc tcc ttc gag gtc 163
 Asp Leu Thr Val Gly Asn Asn Phe Val His Asn Val Ser Phe Glu Val 20
 10 15 20
 aac ccc ggc gaa cgc gtc ggc atc atc ggc gag tcc ggc tca ggc aaa 211
 Asn Pro Gly Glu Arg Val Gly Ile Ile Gly Glu Ser Gly Ser Gly Lys 35
 25 30 35
 tca ctc acc gcg cta tcc atc atg ggt tta act gac ctg ccg acc acc 259
 Ser Leu Thr Ala Leu Ser Ile Met Gly Leu Thr Asp Leu Pro Thr Thr 50
 40 45 50

ggc cag atc acc ttc aac ggc aaa ccc tcc gct aca ttc cgt ggc acc	307
Gly Gln Ile Thr Phe Asn Gly Lys Pro Ser Ala Thr Phe Arg Gly Thr	
55 60 65	
cgc atc gcc atg gtt ttc caa gaa cca atg agc gca ctc aac ccg ctc	355
Arg Ile Ala Met Val Phe Gln Glu Pro Met Ser Ala Leu Asn Pro Leu	
70 75 80 85	
atg cgc atc ggc cgc caa atc gaa gaa atg atg acc ctg cac ggg gca	403
Met Arg Ile Gly Arg Gln Ile Glu Glu Met Met Thr Leu His Gly Ala	
90 95 100	
agc aaa aaa gac gcg cgg gcg cgc tta aaa agc ttg ctt atc gac gtc	451
Ser Lys Lys Asp Ala Arg Ala Arg Leu Lys Ser Leu Leu Ile Asp Val	
105 110 115	
tcc ctc ccc gaa cgc acc gct tcg gcc tac cca cac gaa ctt tca ggc	499
Ser Leu Pro Glu Arg Thr Ala Ser Ala Tyr Pro His Glu Leu Ser Gly	
120 125 130	
ggg caa cgc caa cgc gca cta atc gca atg gcg ctg gcc aat gat cct	547
Gly Gln Arg Gln Arg Ala Leu Ile Ala Met Ala Leu Ala Asn Asp Pro	
135 140 145	
gac ctg ttg atc tgc gat gaa ccc acc acg gct ttg gat gtg gtt gtg	595
Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp Val Val Val	
150 155 160 165	
caa aaa caa atc gtc gat ctg ctg ctg cgt ctc acc aaa gaa cgt ggc	643
Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys Glu Arg Gly	
170 175 180	
acc gct tta ttg ttc atc acc cac gat ctt gga ctc atc gcg cgc acc	691
Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile Ala Arg Thr	
185 190 195	
tgc gaa cgc tta ttg gtg atg aaa tcc ggc gaa acc gta gaa cgc ggc	739
Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val Glu Arg Gly	
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gac acc gag gca att ctt cgc tcc ccc gcc cat tcg tat acc caa cag	787
Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr Thr Gln Gln	
215 220 225	
ctc ctt gat gct tca atc ctt gac cag cca gaa atc gcc tca gat tct	835
Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala Ser Asp Ser	
230 235 240 245	
ggc gcg ccg gta gtg att gat gtg gag gag gcg tcg aaa agc ttt aaa	883
Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys Ser Phe Lys	
250 255 260	
gaa acc acc gcc ctc cac aag gtt tca ttg gcg gtg cgc aaa ggt gac	931
Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg Lys Gly Asp	
265 270 275	
ctg ctt gga ata gtc ggc gga tca ggt tcc ggc aaa acg act ctg ctg	979
Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr Thr Leu Leu	
280 285 290	

aag ctc atc gcc ggt ttg gat aag ccc aca acc ggt acc gtt gcg gta 1027
Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr Val Ala Val
295 300 305

acc ggt ggt gtg cag atg gtg ttt cag gat ccc caa tca agc ctc aac 1075
Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser Ser Leu Asn
310 315 320 325

cca cgg atg aaa atc aaa gac att gtc gcc gaa cca ctg ctt ggt tgg 1123
Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu Leu Gly Trp
330 335 340

aac gcg gcg gag aaa acc aca cgg gtt gcg gaa gtc atc acc caa gtg 1171
Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile Thr Gln Val
345 350 355

gga ctg agc ccc gat gtc tta gat cgc tac ccc cac gaa ttc tcc gga 1219
Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu Phe Ser Gly
360 365 370

gga cag cgc caa cga atc tcc atc gcc aga gcc ctc gcc atc aaa cca 1267
Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala Ile Lys Pro
375 380 385

gcg atc ctg ctt gcc gac gaa cct gtc tcc gcc ctc gat gtg tcc gta 1315
Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp Val Ser Val
390 395 400 405

cgt aaa caa gta ctg gat ctt ctc caa caa ctc gtc gaa gaa tac ggc 1363
Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu Val Glu Glu Tyr Gly
410 415 420

atc acc ttg gtg ttc gtc tcc cac gat ctg gca gtg gtg aga cac ctg 1411
Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val Arg His Leu
425 430 435

tgc aca acc gtg tgg gtg atg gaa cag gga cga gtc ctt gag caa ggg 1459
Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu Glu Gln Gly
440 445 450

ccc atc gat tcg gtt tat gat cac cca cag acc gaa tac acc aag gag 1507
Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr Thr Lys Glu
455 460 465

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Leu Leu Asp Ala Val Pro Arg Leu Ser Leu
470 475

cgc 1560

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<212> PRT
<213> Corynebacterium glutamicum

<400> 130
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 35 40 45
 Asp Leu Pro Thr Thr Gly Gln Ile Thr Phe Asn Gly Lys Pro Ser Ala
 50 55 60
 Thr Phe Arg Gly Thr Arg Ile Ala Met Val Phe Gln Glu Pro Met Ser
 65 70 75 80
 Ala Leu Asn Pro Leu Met Arg Ile Gly Arg Gln Ile Glu Glu Met Met
 85 90 95
 Thr Leu His Gly Ala Ser Lys Lys Asp Ala Arg Ala Arg Leu Lys Ser
 100 105 110
 Leu Leu Ile Asp Val Ser Leu Pro Glu Arg Thr Ala Ser Ala Tyr Pro
 115 120 125
 His Glu Leu Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Met Ala
 130 135 140
 Leu Ala Asn Asp Pro Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala
 145 150 155 160
 Leu Asp Val Val Val Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu
 165 170 175
 Thr Lys Glu Arg Gly Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly
 180 185 190
 Leu Ile Ala Arg Thr Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu
 195 200 205
 Thr Val Glu Arg Gly Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His
 210 215 220
 Ser Tyr Thr Gln Gln Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu
 225 230 235 240
 Ile Ala Ser Asp Ser Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala
 245 250 255
 Ser Lys Ser Phe Lys Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala
 260 265 270
 Val Arg Lys Gly Asp Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly
 275 280 285
 Lys Thr Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr
 290 295 300
 Gly Thr Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro
 305 310 315 320
 Gln Ser Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu
 325 330 335
 Pro Leu Leu Gly Trp Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu
 340 345 350

gaa cgc ggc gac acc gag gca att ctt cgc tcc ccc gcc cat tcg tat	336
Glu Arg Gly Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr	
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acc caa cag ctc ctt gat gct tca atc ctt gac cag cca gaa atc gcc	384
Thr Gln Gln Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala	
115 120 125	
tca gat tct ggc gcg ccg gta gtg att gat gtg gag gag gcg tcg aaa	432
Ser Asp Ser Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys	
130 135 140	
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Ser Phe Lys Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg	
145 150 155 160	
aaa ggt gac ctg ctt gga ata gtc ggc gga tca ggt tcc gcc aaa acg	528
Lys Gly Asp Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr	
165 170 175	
act ctg ctg aag ctc atc gcc ggt ttg gat aag ccc aca acc ggt acc	576
Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr	
180 185 190	
gtt gcg gta acc ggt ggt gtg cag atg gtg ttt cag gat ccc caa tca	624
Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser	
195 200 205	
agc ctc aac cca cgg atg aaa atc aaa gac att gtc gcc gaa cca ctg	672
Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu	
210 215 220	
ctt ggt tgg aac gcg gcg gag aaa acc aca cgg gtt gcg gaa gtc atc	720
Leu Gly Trp Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile	
225 230 235 240	
acc caa gtg gga ctg agc ccc gat gtc tta gat cgc tac ccc cac gaa	768
Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu	
245 250 255	
ttc tcc gga gga cag cgc caa cga atc tcc atc gcc aga gcc ctc gcc	816
Phe Ser Gly Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala	
260 265 270	
atc aaa cca gcg atc ctg ctt gcc gac gaa cct gtc tcc gcc ctc gat	864
Ile Lys Pro Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp	
275 280 285	
gtg tcc gta cgt aaa caa gta ctg gat ctt ctc caa caa ctc gtc gaa	912
Val Ser Val Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu Val Glu	
290 295 300	
gaa tac ggc atc acc ttg gtg ttc gtc tcc cac gat ctg gca gtg gtg	960
Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val	
305 310 315 320	
aga cac ctg tgc aca acc gtg tgg gtg atg gaa cag gga cga gtc ctt	1008
Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu	
325 330 335	
gag caa ggg ccc atc gat tcg gtt tat gat cac cca cag acc gaa tac	1056

Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr
 340 345 350

acc aag gag ctg ctt gat gcc gtt ccg cgg ttg agc ctt taaaccagcg 1105
 Thr Lys Glu Leu Leu Asp Ala Val Pro Arg Leu Ser Leu
 355 360 365

cagatgacaa cgc 1118

<210> 132

<211> 365

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

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 20 25 30

Asn Asp Pro Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp
 35 40 45

Val Val Val Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys
 50 55 60

Glu Arg Gly Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile
 65 70 75 80

Ala Arg Thr Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val
 85 90 95

Glu Arg Gly Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr
 100 105 110

Thr Gln Gln Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala
 115 120 125

Ser Asp Ser Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys
 130 135 140

Ser Phe Lys Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg
 145 150 155 160

Lys Gly Asp Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr
 165 170 175

Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr
 180 185 190

Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser
 195 200 205

Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu
 210 215 220

Leu Gly Trp Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile
 225 230 235 240

Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu
 245 250 255
 Phe Ser Gly Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala
 260 265 270
 Ile Lys Pro Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp
 275 280 285
 Val Ser Val Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu Val Glu
 290 295 300
 Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val
 305 310 315 320
 Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu
 325 330 335
 Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr
 340 345 350
 Thr Lys Glu Leu Leu Asp Ala Val Pro Arg Leu Ser Leu
 355 360 365

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 <211> 1854
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1831)
 <223> RXN01939

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 atgtcgtccg cgacgctctg gatactaagt cgaggaagcg atg acc acc aac atc 115
 Met Thr Thr Asn Ile
 1 5
 cca caa acc ccc aac cac gag ggt gaa cag cca ctg ctc gag ctg aag 163
 Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro Leu Leu Glu Leu Lys
 10 15 20
 gat cta aag att tcc ttc acc tcc tcc acc ggt gtt gtc gac gct gtc 211
 Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly Val Val Asp Ala Val
 25 30 35
 cgt ggc gca aac ctc acc att tat cct ggc caa tct gtt gcc atc gtg 259
 Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln Ser Val Ala Ile Val
 40 45 50
 ggt gaa tcc ggt tca ggt aaa tcg acc acg gca atg tcg atc atc ggt 307
 Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Met Ser Ile Ile Gly
 55 60 65
 ctg ctt cca ggc acc ggc aaa gtg acc gaa ggt tcc atc atg ttt gat 355
 Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly Ser Ile Met Phe Asp
 70 75 80 85

ggc caa gac atc aca ggc ttg agt aac aag cag atg gaa aag tac cgc 403
 Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln Met Glu Lys Tyr Arg
 90 95 100

ggt tca gaa atc gga ctg gtc ccc cag gat ccg atg acc aac ttg aac 451
 Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro Met Thr Asn Leu Asn
 105 110 115

ccg gtg tgg cgc atc ggc acc cag gtc aag gaa tcc ctc cga gcc aac 499
 Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu Ser Leu Arg Ala Asn
 120 125 130

cac gtg gtt cca ggc tca gag atg gac aag cgc gtg gca gaa gtt ctg 547
 His Val Val Pro Gly Ser Glu Met Asp Lys Arg Val Ala Glu Val Leu
 135 140 145

gcc gag gca ggt ctt cct gat gct gag cgt cgc gca aag cag tac cca 595
 Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg Ala Lys Gln Tyr Pro
 150 155 160 165

cat gag ttc tct ggc ggt atg cgc cag cgc gca ctg atc gcc att ggt 643
 His Glu Phe Ser Gly Gly Met Arg Gln Arg Ala Leu Ile Ala Ile Gly
 170 175 180

ttg gcg gca cgc ccg aag ctc ttg atc gcc gac gag ccc acc tct gcg 691
 Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp Glu Pro Thr Ser Ala
 185 190 195

ctg gat gtc acc gtg cag cgc caa atc ctt gat cac ctt gaa aca ctg 739
 Leu Asp Val Thr Val Gln Arg Gln Ile Leu Asp His Leu Glu Thr Leu
 200 205 210

acc aag gat ctc ggc acc gca gtg cta ttt att acc cac gac ttg ggc 787
 Thr Lys Asp Leu Gly Thr Ala Val Leu Phe Ile Thr His Asp Leu Gly
 215 220 225

ctt gcc gct gag cgc gcg gag cac ctc gtg gtg atg cac cgc gga cgc 835
 Leu Ala Ala Glu Arg Ala Glu His Leu Val Val Met His Arg Gly Arg
 230 235 240 245

atc gtg gag tcc ggc cca tca ttg aag att ctg cgc aat cca cag cac 883
 Ile Val Glu Ser Gly Pro Ser Leu Lys Ile Leu Arg Asn Pro Gln His
 250 255 260

cca tat acc caa cgc ttg gtt aag gct gcg ccg tct ctg gct tct gca 931
 Pro Tyr Thr Gln Arg Leu Val Lys Ala Ala Pro Ser Leu Ala Ser Ala
 265 270 275

cgt att caa agt gcg cag gaa caa ggc att gaa tct gca gaa ctg ctc 979
 Arg Ile Gln Ser Ala Gln Glu Gln Gly Ile Glu Ser Ala Glu Leu Leu
 280 285 290

tct gca acg gcc gtt gct gag ggc act att cca gag atg gaa gaa aaa 1027
 Ser Ala Thr Ala Val Ala Glu Gly Thr Ile Pro Glu Met Glu Glu Lys
 295 300 305

gtt atc gag gtg aaa aac ctc acc cgc gaa ttt gat atc cgc ggt gcc 1075
 Val Ile Glu Val Lys Asn Leu Thr Arg Glu Phe Asp Ile Arg Gly Ala
 310 315 320 325

GENE TEE 669

cgt ggc gat aag aag aag ctg aag gcc gtt gat gat gtg tcc ttc ttc	1123
Arg Gly Asp Lys Lys Lys Leu Lys Ala Val Asp Asp Val Ser Phe Phe	
330 335 340	
gta cgt aaa ggc acc acc acc gca ctt gtg ggt gaa tcc ggt tcg ggt	1171
Val Arg Lys Gly Thr Thr Thr Ala Leu Val Gly Glu Ser Gly Ser Gly	
345 350 355	
aaa tcc acc gtg gcc aac atg gtg ctc aac ctt ctc gag cca acc agc	1219
Lys Ser Thr Val Ala Asn Met Val Leu Asn Leu Leu Glu Pro Thr Ser	
360 365 370	
gga gag gtg ctc tac aac ggc acc gat ctt acg tcc ttg agc cac aag	1267
Gly Glu Val Leu Tyr Asn Gly Thr Asp Leu Thr Ser Leu Ser His Lys	
375 380 385	
gaa atc ttc caa atg cga cgc aaa ctg cag gtg gtg ttc cag aac ccc	1315
Glu Ile Phe Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro	
390 395 400 405	
tac ggc tcg ctt gat ccg atg tac tcc atc tac cgg tgt att gag gaa	1363
Tyr Gly Ser Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu	
410 415 420	
ccg ctg acc atc cac aag gtt ggt gga gac cgc aag gca cgc gaa gct	1411
Pro Leu Thr Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala	
425 430 435	
cgc gtc gct gaa ctt ctc gat atg gtg tcc atg ccc agg tcc acc atg	1459
Arg Val Ala Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met	
440 445 450	
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Arg Arg Tyr Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala	
455 460 465	
atc gcc cgt gca ttg gca ctg aat cca gaa gtg atc gtg ttg gat gaa	1555
Ile Ala Arg Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu	
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Ala Val Ser Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu	
490 495 500	
ctt gca gaa ctt cag cag gaa ctg aag ctc acc tat ttg ttc atc acc	1651
Leu Ala Glu Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr	
505 510 515	
cac gac ttg gcc gtt gtt cga caa acc gcc gac gat gtt gtg gtg atg	1699
His Asp Leu Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Met	
520 525 530	
caa aag gga cga atc gtt gaa aag ggt cgt acc gac gac atc ttc aac	1747
Gln Lys Gly Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn	
535 540 545	
gat cct cag cag cac tac acc cgc gat ttg atc aat gcg gta cct ggt	1795
Asp Pro Gln Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly	
550 555 560 565	
ctg gga atc gag ttg ggt act gga gaa aac ctg gtt taaccgcgac	1841

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570 575

agcctcacta aac

1854

<210> 134

<211> 577

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

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20 25 30

Val Val Asp Ala Val Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln
35 40 45

Ser Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala
50 55 60

Met Ser Ile Ile Gly Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly
65 70 75 80

Ser Ile Met Phe Asp Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln
85 90 95

Met Glu Lys Tyr Arg Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro
100 105 110

Met Thr Asn Leu Asn Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu
115 120 125

Ser Leu Arg Ala Asn His Val Val Pro Gly Ser Glu Met Asp Lys Arg
130 135 140

Val Ala Glu Val Leu Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg
145 150 155 160

Ala Lys Gln Tyr Pro His Glu Phe Ser Gly Gly Met Arg Gln Arg Ala
165 170 175

Leu Ile Ala Ile Gly Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp
180 185 190

Glu Pro Thr Ser Ala Leu Asp Val Thr Val Gln Arg Gln Ile Leu Asp
195 200 205

His Leu Glu Thr Leu Thr Lys Asp Leu Gly Thr Ala Val Leu Phe Ile
210 215 220

Thr His Asp Leu Gly Leu Ala Ala Glu Arg Ala Glu His Leu Val Val
225 230 235 240

Met His Arg Gly Arg Ile Val Glu Ser Gly Pro Ser Leu Lys Ile Leu
245 250 255

Arg Asn Pro Gln His Pro Tyr Thr Gln Arg Leu Val Lys Ala Ala Pro

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<222> (101)..(691)
<223> FRXA00761
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Met Thr Thr Asn Ile																	5
1																	
cca caa acc ccc aac cac gag ggt gaa cag cca ctg ctc gag ctg aag																	163
Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro Leu Leu Glu Leu Lys																	20
10 15																	
gat cta aag att tcc ttc acc tcc tcc acc ggt gtt gtc gac gct gtc																	211
Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly Val Val Asp Ala Val																	35
25 30																	
cgt ggc gca aac ctc acc att tat cct ggc caa tct gtt gcc atc gtg																	259
Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln Ser Val Ala Ile Val																	50
40 45																	
ggg gaa tcc ggt tca ggt aaa tcg acc acg gca atg tcg atc atc ggt																	307
Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Met Ser Ile Ile Gly																	65
55 60																	
ctg ctt cca ggc acc ggc aaa gtg acc gaa ggt tcc atc atg ttt gat																	355
Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly Ser Ile Met Phe Asp																	85
70 75 80																	
ggc caa gac atc aca ggc ttg agt aac aag cag atg gaa aag tac cgc																	403
Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln Met Glu Lys Tyr Arg																	100
90 95 100																	
ggg tca gaa atc gga ctg gtc ccc cag gat ccg atg acc aac ttg aac																	451
Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro Met Thr Asn Leu Asn																	115
105 110																	
ccg gtg tgg cgc atc ggc acc cag gtc aag gaa tcc ctc cga gcc aac																	499
Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu Ser Leu Arg Ala Asn																	130
120 125 130																	
cac gtg gtt cca ggc tca gag atg gac aag cgc gtg gca gaa gtt ctg																	547
His Val Val Pro Gly Ser Glu Met Asp Lys Arg Val Ala Glu Val Leu																	145
135 140 145																	
gcc gag gca ggt ctt cct gat gct gag cgt cgc gca aag cag tac cca																	595
Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg Ala Lys Gln Tyr Pro																	165
150 155 160																	
cat gag ttc tct ggc ggt atg cgc cac cgc gca ctg atc gcc att ggt																	643
His Glu Phe Ser Gly Gly Met Arg His Arg Ala Leu Ile Ala Ile Gly																	

170	175	180	
ttg gcg gca cgc ccg aag ctc ttg atc gcc gac gag ccc acc tct gcg			691
Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp Glu Pro Thr Ser Ala			
185	190	195	

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 136
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 Leu Leu Glu Leu Lys Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly
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 Val Val Asp Ala Val Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln
 35 40 45
 Ser Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala
 50 55 60
 Met Ser Ile Ile Gly Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly
 65 70 75 80
 Ser Ile Met Phe Asp Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln
 85 90 95
 Met Glu Lys Tyr Arg Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro
 100 105 110
 Met Thr Asn Leu Asn Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu
 115 120 125
 Ser Leu Arg Ala Asn His Val Val Pro Gly Ser Glu Met Asp Lys Arg
 130 135 140
 Val Ala Glu Val Leu Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg
 145 150 155 160
 Ala Lys Gln Tyr Pro His Glu Phe Ser Gly Gly Met Arg His Arg Ala
 165 170 175
 Leu Ile Ala Ile Gly Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp
 180 185 190
 Glu Pro Thr Ser Ala
 195

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(603)

<223> FRXA01939

<400> 137

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Ser	Thr	Ser	Gly	Thr	Asp	Leu	Thr	Ser	Leu	Ser	His	Lys	Glu	Ile	Phe	
1				5				10						15		
caa	atg	cga	cgc	aaa	ctg	cag	gtg	gtg	ttc	cag	aac	ccc	tac	ggc	tcg	96
Gln	Met	Arg	Arg	Lys	Leu	Gln	Val	Val	Phe	Gln	Asn	Pro	Tyr	Gly	Ser	
			20				25					30				
ctt	gat	ccg	atg	tac	tcc	atc	tac	cgg	tgt	att	gag	gaa	ccg	ctg	acc	144
Leu	Asp	Pro	Met	Tyr	Ser	Ile	Tyr	Arg	Cys	Ile	Glu	Glu	Pro	Leu	Thr	
		35				40					45					
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Ile	His	Lys	Val	Gly	Gly	Asp	Arg	Lys	Ala	Arg	Glu	Ala	Arg	Val	Val	
	50				55					60						
gaa	ctt	ctc	gat	atg	gtg	tcc	atg	ccc	agg	tcc	acc	atg	cgc	cgc	tac	240
Glu	Leu	Leu	Asp	Met	Val	Ser	Met	Pro	Arg	Ser	Thr	Met	Arg	Arg	Tyr	
65					70			75							80	
ccc	aac	gag	ctt	tcc	ggc	ggc	caa	cgt	cag	cgc	atc	gcc	atc	gcc	cgt	288
Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala	Ile	Ala	Arg	
				85				90						95		
gca	ttg	gca	ctg	aat	cca	gaa	gtg	atc	gtg	ttg	gat	gaa	gcg	gtt	tcc	336
Ala	Leu	Ala	Leu	Asn	Pro	Glu	Val	Ile	Val	Leu	Asp	Glu	Ala	Val	Ser	
			100				105						110			
gct	ttg	gac	gtg	ttg	gtt	cag	aac	cag	atc	ctc	acc	ctg	ctt	gca	gaa	384
Ala	Leu	Asp	Val	Leu	Val	Gln	Asn	Gln	Ile	Leu	Thr	Leu	Leu	Ala	Glu	
		115				120						125				
ctt	cag	cag	gaa	ctg	aag	ctc	acc	tat	ttg	ttc	atc	acc	cac	gac	ttg	432
Leu	Gln	Gln	Glu	Leu	Lys	Leu	Thr	Tyr	Leu	Phe	Ile	Thr	His	Asp	Leu	
	130					135					140					
gcc	gtt	gtt	cga	caa	acc	gcc	gac	gat	gtt	gtg	gtg	atg	caa	aag	gga	480
Ala	Val	Val	Arg	Gln	Thr	Ala	Asp	Asp	Val	Val	Val	Met	Gln	Lys	Gly	
145					150					155				160		
cga	atc	gtt	gaa	aag	ggc	cgt	acc	gac	gac	atc	ttc	aac	gat	cct	cag	528
Arg	Ile	Val	Glu	Lys	Gly	Arg	Thr	Asp	Asp	Ile	Phe	Asn	Asp	Pro	Gln	
				165				170						175		
cag	cac	tac	acc	cgc	gat	ttg	atc	aat	gcg	gta	cct	ggc	ctg	gga	atc	576
Gln	His	Tyr	Thr	Arg	Asp	Leu	Ile	Asn	Ala	Val	Pro	Gly	Leu	Gly	Ile	
			180					185					190			
gag	ttg	ggc	act	gga	gaa	aac	ctg	gtt	taacccgcac	agcctcacta						623
Glu	Leu	Gly	Thr	Gly	Glu	Asn	Leu	Val								
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aac																626

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<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

Ser Thr Ser Gly Thr Asp Leu Thr Ser Leu Ser His Lys Glu Ile Phe
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Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro Tyr Gly Ser
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Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu Pro Leu Thr
35 40 45

Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala Arg Val Val
50 55 60

Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met Arg Arg Tyr
65 70 75 80

Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg
85 90 95

Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu Ala Val Ser
100 105 110

Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu Leu Ala Glu
115 120 125

Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr His Asp Leu
130 135 140

Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Val Met Gln Lys Gly
145 150 155 160

Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn Asp Pro Gln
165 170 175

Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly Leu Gly Ile
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Glu Leu Gly Thr Gly Glu Asn Leu Val
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<210> 139

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<212> DNA

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<222> (101)..(1024)

<223> RXN00759

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Met Leu Arg Tyr Val
1 5

ggg cga cgt ttg ctc caa atg att ccg gtc ttt ttc gga gcg acc tta 163

Gly	Arg	Arg	Leu	Leu	Gln	Met	Ile	Pro	Val	Phe	Phe	Gly	Ala	Thr	Leu		
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ctg	att	tac	gcc	ctc	gtg	ttc	ctc	atg	cct	ggg	gac	cca	gtc	cag	gca	211	
Leu	Ile	Tyr	Ala	Leu	Val	Phe	Leu	Met	Pro	Gly	Asp	Pro	Val	Gln	Ala		
			25					30					35				
ttg	gga	ggg	gac	cgc	ggc	cta	acc	gag	gct	gcg	gcc	gag	aaa	atc	cgt	259	
Leu	Gly	Gly	Asp	Arg	Gly	Leu	Thr	Glu	Ala	Ala	Ala	Glu	Lys	Ile	Arg		
			40				45					50					
caa	gaa	tac	aat	ctt	gat	aaa	ccc	ttc	atc	gtt	caa	tac	ctc	ctg	tac	307	
Gln	Glu	Tyr	Asn	Leu	Asp	Lys	Pro	Phe	Ile	Val	Gln	Tyr	Leu	Leu	Tyr		
			55			60					65						
atc	aag	ggc	atc	ttc	gtc	tta	gat	ttt	gga	aca	acc	ttc	tct	ggg	cag	355	
Ile	Lys	Gly	Ile	Phe	Val	Leu	Asp	Phe	Gly	Thr	Thr	Phe	Ser	Gly	Gln		
			70		75					80					85		
cca	gtt	att	gat	gtg	atg	gcc	agg	gcc	ttc	ccc	gtc	acc	atc	aaa	ctc	403	
Pro	Val	Ile	Asp	Val	Met	Ala	Arg	Ala	Phe	Pro	Val	Thr	Ile	Lys	Leu		
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gcc	atc	atg	gcc	ctg	ctg	ttt	gaa	tca	atc	ctc	ggc	att	atc	ttt	ggg	451	
Ala	Ile	Met	Ala	Leu	Leu	Phe	Glu	Ser	Ile	Leu	Gly	Ile	Ile	Phe	Gly		
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gtc	atc	gca	ggg	att	cgc	cgc	gga	gga	atc	ttc	gac	tcc	acc	gtg	ctg	499	
Val	Ile	Ala	Gly	Ile	Arg	Arg	Gly	Gly	Ile	Phe	Asp	Ser	Thr	Val	Leu		
			120				125					130					
gtc	ctt	tct	ctg	ata	gtc	atc	gca	gtc	ccc	acc	ttc	gtc	att	ggg	ttc	547	
Val	Leu	Ser	Leu	Ile	Val	Ile	Ala	Val	Pro	Thr	Phe	Val	Ile	Gly	Phe		
			135			140					145						
gtg	ctg	cag	ttc	tta	gtc	ggc	gtg	aaa	tgg	ggc	tta	ctg	ccc	gtc	acc	595	
Val	Leu	Gln	Phe	Leu	Val	Gly	Val	Lys	Trp	Gly	Leu	Leu	Pro	Val	Thr		
					155				160					165			
gta	ggg	tcc	aac	aca	tca	ata	acg	gcg	ctg	atc	atg	cgg	gct	gtc	gta	643	
Val	Gly	Ser	Asn	Thr	Ser	Ile	Thr	Ala	Leu	Ile	Met	Pro	Ala	Val	Val		
				170				175						180			
ctg	ggg	gca	gta	tgc	ttc	gcc	tac	gtt	ctt	cgc	ctc	acc	aga	caa	tcc	691	
Leu	Gly	Ala	Val	Ser	Phe	Ala	Tyr	Val	Leu	Arg	Leu	Thr	Arg	Gln	Ser		
			185					190					195				
gtg	agc	gaa	aac	ctc	cgc	gct	gat	tac	gtt	cga	acc	gct	cga	gca	aaa	739	
Val	Ser	Glu	Asn	Leu	Arg	Ala	Asp	Tyr	Val	Arg	Thr	Ala	Arg	Ala	Lys		
			200				205					210					
ggc	atg	tcc	gga	ttc	aac	gtg	atg	aac	cgc	cat	gtg	ctt	cga	aac	tca	787	
Gly	Met	Ser	Gly	Phe	Asn	Val	Met	Asn	Arg	His	Val	Leu	Arg	Asn	Ser		
			215			220					225						
ctg	att	ccc	gtt	gcc	acc	ttc	ctg	ggc	gcc	gat	ctc	ggg	gca	ctg	atg	835	
Leu	Ile	Pro	Val	Ala	Thr	Phe	Leu	Gly	Ala	Asp	Leu	Gly	Ala	Leu	Met		
			230		235					240				245			
ggg	gga	gcg	att	gtc	acc	gaa	ggg	atc	ttc	ggc	atc	aac	ggg	gtc	ggg	883	
Gly	Gly	Ala	Ile	Val	Thr	Glu	Gly	Ile	Phe	Gly	Ile	Asn	Gly	Val	Gly		

Thr Ala Arg Ala Lys Gly Met Ser Gly Phe Asn Val Met Asn Arg His
 210 215 220
 Val Leu Arg Asn Ser Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp
 225 230 235 240
 Leu Gly Ala Leu Met Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly
 245 250 255
 Ile Asn Gly Val Gly Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu
 260 265 270
 Pro Thr Thr Val Val Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile
 275 280 285
 Ile Ala Asn Leu Leu Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg
 290 295 300
 Ile Arg Tyr Ala
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 <223> FRXA00759

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 Met Leu Arg Tyr Val
 1 5
 ggg cga cgt ttg ctc caa atg att ccg gtc ttt ttc gga gcg acc tta 163
 Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe Phe Gly Ala Thr Leu
 10 15 20
 ctg att tac gcc ctc gtg ttc ctc atg cct ggt gac cca gtc cag gca 211
 Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly Asp Pro Val Gln Ala
 25 30 35
 ttg gga ggt gac cgc ggc cta acc gag gct gcg gcc gag aaa atc cgt 259
 Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala Ala Glu Lys Ile Arg
 40 45 50
 caa gaa tac aat ctt gat aaa ccc ttc atc gtt caa tac ctc ctg tac 307
 Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val Gln Tyr Leu Leu Tyr
 55 60 65
 atc aag ggc atc ttc gtc tta gat ttt gga aca acc ttc tct ggt cag 355
 Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr Thr Phe Ser Gly Gln
 70 75 80 85
 cca gtt att gat gtg atg gcc agg gcc ttc ccc gtc acc atc aaa ctc 403

Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro Val Thr Ile Lys Leu
 90 95 100

gcc atc atg gcc ctg ctg ttt gaa tca atc ctc ggc att atc ttt ggt 451
 Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu Gly Ile Ile Phe Gly
 105 110 115

gtc atc gca ggt att cgc cgc gga gga atc ttc gac tcc acc gtg ctg 499
 Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe Asp Ser Thr Val Leu
 120 125 130

gtc ctt tct ctg ata gtc atc gca gtc ccc acc ttc gtc att ggt ttc 547
 Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr Phe Val Ile Gly Phe
 135 140 145

gtg ctg cag ttc tta ntc ggc gtg aaa tgg ggc tta ctg ccc gtc acc 595
 Val Leu Gln Phe Leu Xaa Gly Val Lys Trp Gly Leu Leu Pro Val Thr
 150 155 160 165

gta ggt tcc aac aca tca ata acg gcg ctg atc atg ccg gct gtc gta 643
 Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile Met Pro Ala Val Val
 170 175 180

ctg ggt gca gta tct ttc gcc tac gtt ctt cgc ctc acc aga caa tcc 691
 Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg Leu Thr Arg Gln Ser
 185 190 195

gtg agc gaa aac ctc cgc gct gat tac gtt cga acc gct cga gca aaa 739
 Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg Thr Ala Arg Ala Lys
 200 205 210

ggc atg tcc gga ttc aac gtg atg aac cgc cat gtg ctt cga aac tca 787
 Gly Met Ser Gly Phe Asn Val Met Asn Arg His Val Leu Arg Asn Ser
 215 220 225

ctg att ccc gtt gcc acc ttc ctg ggc gcc gat ctc ggt gca ctg atg 835
 Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp Leu Gly Ala Leu Met
 230 235 240 245

ggt gga gcg att gtc acc gaa ggt atc ttc ggc atc aac ggt gtc ggt 883
 Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly Ile Asn Gly Val Gly
 250 255 260

gga acg ctc tac cag gcc att ttg aaa ggt gaa ccc acc acg gtt gtc 931
 Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu Pro Thr Thr Val Val
 265 270 275

tcc att gtc act gtg ctg gtc atc gtc tac atc atc gcc aac ctt ctc 979
 Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile Ile Ala Asn Leu Leu
 280 285 290

gtg gac ttg atc tac gcc gtt ctc gat ccg agg atc cgc tat gcc 1024
 Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg Ile Arg Tyr Ala
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<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

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 Phe Gly Ala Thr Leu Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly
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 Asp Pro Val Gln Ala Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala
 35 40 45
 Ala Glu Lys Ile Arg Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val
 50 55 60
 Gln Tyr Leu Leu Tyr Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr
 65 70 75 80
 Thr Phe Ser Gly Gln Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro
 85 90 95
 Val Thr Ile Lys Leu Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu
 100 105 110
 Gly Ile Ile Phe Gly Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe
 115 120 125
 Asp Ser Thr Val Leu Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr
 130 135 140
 Phe Val Ile Gly Phe Val Leu Gln Phe Leu Xaa Gly Val Lys Trp Gly
 145 150 155 160
 Leu Leu Pro Val Thr Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile
 165 170 175
 Met Pro Ala Val Val Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg
 180 185 190
 Leu Thr Arg Gln Ser Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg
 195 200 205
 Thr Ala Arg Ala Lys Gly Met Ser Gly Phe Asn Val Met Asn Arg His
 210 215 220
 Val Leu Arg Asn Ser Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp
 225 230 235 240
 Leu Gly Ala Leu Met Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly
 245 250 255
 Ile Asn Gly Val Gly Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu
 260 265 270
 Pro Thr Thr Val Val Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile
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 Ile Ala Asn Leu Leu Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg
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 Ile Arg Tyr Ala

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				Met	Val	Ser	Ile	Asp	5							
				1												
aca	tac	aac	gcc	tgc	gtc	gac	ttc	ccc	atc	ttc	gac	gcc	aaa	tcc	cgc	163
Thr	Tyr	Asn	Ala	Cys	Val	Asp	Phe	Pro	Ile	Phe	Asp	Ala	Lys	Ser	Arg	
			10					15						20		
tcc	atg	aag	aaa	gcc	ttc	ctc	ggc	gca	gcc	ggc	gga	gca	atc	ggg	cgc	211
Ser	Met	Lys	Lys	Ala	Phe	Leu	Gly	Ala	Ala	Gly	Gly	Ala	Ile	Gly	Arg	
			25					30					35			
aat	caa	gac	aac	gtc	gta	gtc	gtc	gaa	gcg	ctg	aag	aac	gtc	aac	ctg	259
Asn	Gln	Asp	Asn	Val	Val	Val	Val	Glu	Ala	Leu	Lys	Asn	Val	Asn	Leu	
		40					45					50				
cac	ttg	cgc	gaa	ggc	gac	cgg	gtc	gga	ctc	gtc	ggc	cac	aac	ggc	gcc	307
His	Leu	Arg	Glu	Gly	Asp	Arg	Val	Gly	Leu	Val	Gly	His	Asn	Gly	Ala	
	55					60					65					
ggc	aaa	tcc	acc	ctc	ctg	cga	ctc	ctc	tcc	ggc	atc	tac	gaa	ccc	acc	355
Gly	Lys	Ser	Thr	Leu	Leu	Arg	Leu	Leu	Ser	Gly	Ile	Tyr	Glu	Pro	Thr	
	70				75				80						85	
cgc	gga	agc	gct	gac	atc	cgt	gga	cgc	gtc	gcc	ccc	gtc	ttc	gac	ctc	403
Arg	Gly	Ser	Ala	Asp	Ile	Arg	Gly	Arg	Val	Ala	Pro	Val	Phe	Asp	Leu	
				90					95					100		
ggc	gtc	ggc	atg	gat	cca	gaa	atc	tcc	ggc	tac	gaa	aat	atc	atc	atc	451
Gly	Val	Gly	Met	Asp	Pro	Glu	Ile	Ser	Gly	Tyr	Glu	Asn	Ile	Ile	Ile	
			105					110					115			
cgc	ggc	ctc	ttc	ctc	ggc	caa	acc	cgc	aaa	cag	atg	aaa	gcc	aaa	atg	499
Arg	Gly	Leu	Phe	Leu	Gly	Gln	Thr	Arg	Lys	Gln	Met	Lys	Ala	Lys	Met	
		120					125					130				
gaa	gaa	atc	gcc	gac	ttc	acc	gaa	ctc	ggc	gaa	tac	ctc	tcc	atg	cct	547
Glu	Glu	Ile	Ala	Asp	Phe	Thr	Glu	Leu	Gly	Glu	Tyr	Leu	Ser	Met	Pro	
	135					140				145						
ctc	cga	acc	tac	tcc	acc	ggc	atg	cgc	atc	cgc	cta	gcc	ctc	ggc	gtg	595
Leu	Arg	Thr	Tyr	Ser	Thr	Gly	Met	Arg	Ile	Arg	Leu	Ala	Leu	Gly	Val	
	150				155					160					165	
gtc	acc	tcc	atc	gag	ccc	gaa	att	ctg	ctt	ctt	gat	gaa	ggc	atc	ggc	643

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male	100%		
Marital status	Married	100%		
Education	High school	100%		
Occupation	Teacher	100%		
Income	1000 TL	100%		
Religion	Islam	100%		
Health status	Good	100%		
Smoking status	Non-smoker	100%		
Alcohol consumption	No	100%		
Stress level	Low	100%		
Sleep quality	Good	100%		
Appetite	Normal	100%		
Weight change	No change	100%		
Blood pressure	Normal	100%		
Blood sugar	Normal	100%		
Cholesterol	Normal	100%		
Triglyceride	Normal	100%		
Hemoglobin	Normal	100%		
Hematocrit	Normal	100%		
White blood cell	Normal	100%		
Platelet	Normal	100%		
Prothrombin time	Normal	100%		
Partial thromboplastin time	Normal	100%		
Fibrinogen	Normal	100%		
D-dimer	Normal	100%		
C-reactive protein	Normal	100%		
Erythrocyte sedimentation rate	Normal	100%		
Urea nitrogen	Normal	100%		
Creatinine	Normal	100%		
Bilirubin	Normal	100%		
Aspartate aminotransferase	Normal	100%		
Alanine aminotransferase	Normal	100%		
Lactate dehydrogenase	Normal	100%		
Procalcitonin	Normal	100%		
Interleukin-6	Normal	100%		
Tumor necrosis factor- α	Normal	100%		
Interleukin-10	Normal	100%		
Interleukin-17	Normal	100%		
Interleukin-22	Normal	100%		
Interleukin-23	Normal	100%		
Interleukin-24	Normal	100%		
Interleukin-25	Normal	100%		
Interleukin-26	Normal	100%		
Interleukin-27	Normal	100%		
Interleukin-28	Normal	100%		
Interleukin-29	Normal	100%		
Interleukin-30	Normal	100%		
Interleukin-31	Normal	100%		
Interleukin-32	Normal	100%		
Interleukin-33	Normal	100%		
Interleukin-34	Normal	100%		
Interleukin-35	Normal	100%		
Interleukin-36	Normal	100%		
Interleukin-37	Normal	100%		
Interleukin-38	Normal	100%		
Interleukin-39	Normal	100%		
Interleukin-40	Normal	100%		
Interleukin-41	Normal	100%		
Interleukin-42	Normal	100%		
Interleukin-43	Normal	100%		
Interleukin-44	Normal	100%		
Interleukin-45	Normal	100%		
Interleukin-46	Normal	100%		
Interleukin-47	Normal	100%		
Interleukin-48	Normal	100%		
Interleukin-49	Normal	100%		
Interleukin-50	Normal	100%		
Interleukin-51	Normal	100%		
Interleukin-52	Normal	100%		
Interleukin-53	Normal	100%		
Interleukin-54	Normal	100%		
Interleukin-55	Normal	100%		
Interleukin-56	Normal	100%		
Interleukin-57	Normal	100%		
Interleukin-58	Normal	100%		
Interleukin-59	Normal	100%		
Interleukin-60	Normal	100%		
Interleukin-61	Normal	100%		
Interleukin-62	Normal	100%		
Interleukin-63	Normal	100%		
Interleukin-64	Normal	100%		
Interleukin-65	Normal	100%		
Interleukin-66	Normal	100%		
Interleukin-67	Normal	100%		
Interleukin-68	Normal	100%		
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Interleukin-70	Normal	100%		
Interleukin-71	Normal	100%		
Interleukin-72	Normal	100%		
Interleukin-73				

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			20					25					30		
Gly	Ala	Ile	Gly	Arg	Asn	Gln	Asp	Asn	Val	Val	Val	Val	Glu	Ala	Leu
		35					40					45			
Lys	Asn	Val	Asn	Leu	His	Leu	Arg	Glu	Gly	Asp	Arg	Val	Gly	Leu	Val
	50					55					60				
Gly	His	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Leu	Arg	Leu	Leu	Ser	Gly
65					70					75					80
Ile	Tyr	Glu	Pro	Thr	Arg	Gly	Ser	Ala	Asp	Ile	Arg	Gly	Arg	Val	Ala
				85					90					95	
Pro	Val	Phe	Asp	Leu	Gly	Val	Gly	Met	Asp	Pro	Glu	Ile	Ser	Gly	Tyr
			100					105					110		
Glu	Asn	Ile	Ile	Ile	Arg	Gly	Leu	Phe	Leu	Gly	Gln	Thr	Arg	Lys	Gln
		115					120					125			
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Thr Arg Met Glu Glu Glu Lys
260

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Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly Ile Tyr Glu Pro Thr
70 75 80 85

cgc gga agc gct gac atc cgt gga cgc gtc gcc ccc gtc ttc gac ctc 403
 Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala Pro Val Phe Asp Leu
 90 95 100
 ggc gtc ggc atg gat cca gaa atc tcc ggc tac gaa aat atc atc atc 451
 Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr Glu Asn Ile Ile Ile
 105 110 115
 cgc ggc ctc ttc ctc ggt caa acc cgc aaa cag atg aaa gcc aaa atg 499
 Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln Met Lys Ala Lys Met
 120 125 130
 gaa gaa atc gcc gac ttc acc gaa ctc ggc gaa tac ctc tcc atg cct 547
 Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu Tyr Leu Ser Met Pro
 135 140 145
 ctc cga acc tac tcc acc ggc atg cgc atc cgc cta gcc ctc ggc gtg 595
 Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg Leu Ala Leu Gly Val
 150 155 160 165
 gtc acc tcc atc gag ccc gaa att ctg ctt ctt gat gaa ggc atc ggc 643
 Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu Asp Glu Gly Ile Gly
 170 175 180
 gcc gtc gac gcc gcc ttc atg gcc aaa gcc cgc gac cgg ctc caa gcc 691
 Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg Asp Arg Leu Gln Ala
 185 190 195
 ctc gtc gaa cga tcc ggc atc ctc gtc ttc gcc tcc act caa cga ctt 739
 Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala Ser Thr Gln Arg Leu
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<211> 225

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<213> Corynebacterium glutamicum

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 35 40 45
 Lys Asn Val Asn Leu His Leu Arg Glu Gly Asp Arg Val Gly Leu Val
 50 55 60
 Gly His Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly
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 85 90 95

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225

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<223> RXN00732
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Gly	Val	Val	Thr	Gly	Asp	Ile	Gly	Tyr	Ile	Trp	His	Thr	Gly	Gly	Ile	
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Met	Leu	Ala	Leu	Thr	Leu	Val	Gln	Val	Ala	Cys	Ala	Ile	Ala	Gly	Val	
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Tyr	Phe	Gly	Ser	Lys	Leu	Ser	Met	Arg	Val	Gly	Arg	Asp	Leu	Arg	Ser	
	50					55					60					
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Ala	Ile	Phe	Gly	Lys	Val	Val	Asn	Phe	Ser	Glu	Arg	Glu	Met	Gly	Gln	
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gtt cct agg ctt ttc gac gtc acc gaa ggc gac gtt acc gtc gat ggc Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly 355 360 365			1104
acc gat gtt cgt gaa ttt gag ccg ctg aag ctg tgg gat cgg atc ggt Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly 370 375 380			1152
ctt gtt ccg cag aag tcg ttc ctg ttt tct gga acg atc gcc agc aac Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn 385 390 395 400			1200
ctg cgt tat ggc aat gaa gat gcc acg gaa acg cag ctg tgg cag gcg Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala 405 410 415			1248
ctt gca att gct cag gcg gcg gac ttt gtg cgt gag atg cca gag ggt Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly 420 425 430			1296
ctt gat tct gag att gct cag ggt gga acc aat gtt tct ggt ggt cag Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln 435 440 445			1344
cgc cag cga cta gcc att gcc agg gcg ttg ttg aag caa cct gag atc Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile 450 455 460			1392
tat att ttc gac gat tct ttc tcc gcc ctc gat gtg agc aca gac gcc Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala 465 470 475 480			1440
gct ctt cgc cga gcg ctg agc acc aac ctg ccg gat gca acc aag ttg Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu 485 490 495			1488
att gtc gcc cag cgt gtc agc acg att cga gat gcc gat cag att gtg Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln Ile Val 500 505 510			1536
gtg ctt gat aac ggc gag gtt gtc ggt att gga acg cac acg aat ttg Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu 515 520 525			1584
ctg aac acg tgc ggt acc tac cgt gaa att gtt gaa tcc caa gag act Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln Glu Thr 530 535 540			1632
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 Ala Ile Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu
 340 345 350
 Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly
 355 360 365
 Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly
 370 375 380
 Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn
 385 390 395 400
 Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala
 405 410 415
 Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly
 420 425 430
 Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln
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 Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile
 450 455 460
 Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala
 465 470 475 480
 Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu
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 Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu
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<223> FRXA00732

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acc	tcc	act	ttg	atg	att	tcc	gcc	ccg	atg	ctg	gcc	att	ggc	ggc	atc	163
Thr	Ser	Thr	Leu	Met	Ile	Ser	Ala	Pro	Met	Leu	Ala	Ile	Gly	Gly	Ile	
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atc	atg	gcg	gtg	cgt	cag	gat	ctt	ggc	ttg	tct	tgg	ctg	atg	gtg	gtc	211
Ile	Met	Ala	Val	Arg	Gln	Asp	Leu	Gly	Leu	Ser	Trp	Leu	Met	Val	Val	
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agt	att	ccg	gtg	ctc	atc	atc	gtg	gtg	gcg	ctg	atc	att	gtg	cgc	atg	259
Ser	Ile	Pro	Val	Leu	Ile	Ile	Val	Val	Ala	Leu	Ile	Ile	Val	Arg	Met	
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Val	Pro	Leu	Phe	Gln	Thr	Met	Gln	Lys	Arg	Ile	Asp	Arg	Ile	Asn	Gln	
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Arg	Glu	Asp	Val	Glu	Arg	Glu	Arg	Phe	Thr	Thr	Ala	Ser	Lys	Asp	Val	
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gct	gat	atc	ggc	gtg	cgc	acc	ggc	aac	ctg	atg	gcg	ttg	atg	ttc	cct	451
Ala	Asp	Ile	Gly	Val	Arg	Thr	Gly	Asn	Leu	Met	Ala	Leu	Met	Phe	Pro	
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gcc	gtg	atg	ctg	atc	atg	aac	ctt	tct	gcc	gtt	gct	gtg	att	tgg	ttt	499
Ala	Val	Met	Leu	Ile	Met	Asn	Leu	Ser	Ala	Val	Ala	Val	Ile	Trp	Phe	
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ggc	gct	ttc	cag	gtg	gaa	tcc	ggc	gag	acg	cag	atc	ggc	acg	ctc	ttt	547
Gly	Ala	Phe	Gln	Val	Glu	Ser	Gly	Glu	Thr	Gln	Ile	Gly	Thr	Leu	Phe	
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gca	ttc	ttg	cag	tac	atc	atg	cag	atc	ctc	atg	ggc	gtc	atg	atg	gca	595
Ala	Phe	Leu	Gln	Tyr	Ile	Met	Gln	Ile	Leu	Met	Gly	Val	Met	Met	Ala	
	150				155					160					165	
gcg	ttc	atg	ttt	gtc	atg	gtt	ccg	cgc	gct	gcc	gtt	tcc	gct	gat	cgc	643
Ala	Phe	Met	Phe	Val	Met	Val	Pro	Arg	Ala	Ala	Val	Ser	Ala	Asp	Arg	
				170					175					180		
atc	ggc	gag	gtt	ctg	gaa	acc	aca	ccg	tct	gtg	cag	gcg	cca	gaa	aca	691
Ile	Gly	Glu	Val	Leu	Glu	Thr	Thr	Pro	Ser	Val	Gln	Ala	Pro	Glu	Thr	
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ccg	gcg	cag	ccg	tcg	aca	agc	gct	ggc	gaa	atc	gtg	ttc	aac	aac	gcg	

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 Phe Arg Val Ala Pro Gly Ser Thr Thr Ala Ile Ile Gly Ser Thr Gly
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<211> 274

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<213> Corynebacterium glutamicum

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 35 40 45

Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys Arg Ile
 50 55 60

Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile Arg Val
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Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe Thr Thr
 85 90 95

Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn Leu Met
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Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser Ala Val
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Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu Thr Gln
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Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile Leu Met
 145 150 155 160

Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg Ala Ala
 165 170 175

Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro Ser Val
 180 185 190

Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly Glu Ile
 195 200 205

Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp Pro Val
 210 215 220

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 Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro Lys Arg Gln Arg Thr Pro
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 Val Gly Asp Leu Ser Gly Gly Glu Arg Arg Arg Leu Gln Leu Thr Arg
 180 185 190
 Val Leu Met Ala Glu Pro Asn Val Leu Leu Leu Asp Glu Pro Thr Asn
 195 200 205
 Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu Glu Ser Leu Leu Asp Gly
 210 215 220
 Trp Pro Gly Thr Met Val Val Ile Ser His Asp Arg Tyr Leu Ile Glu
 225 230 235 240
 Arg Val Thr Asp Ser Thr Trp Ala Leu Phe Gly Asp Gly Lys Leu Thr
 245 250 255
 Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu Gln Arg Arg Ala Ala Met
 260 265 270
 Ala Ala Ala Glu Asp Ser Gly Val Leu Asn Leu Gly Ala Ala Thr Gln
 275 280 285
 Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln Ala Ala Thr Ser Val Glu
 290 295 300
 Ser Ser Gly Ile Ser Ser Gln Glu Arg His Arg Ile Thr Lys Glu Met
 305 310 315 320
 Asn Ala Leu Glu Arg Lys Met Gly Lys Leu Asp Gln Gln Met Asp Lys
 325 330 335
 Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu Ala Met Asp Thr Ile Lys
 340 345 350
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<211> 1142

<212> DNA

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<220>

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<222> (1)..(1119)

<223> FRXA01808

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48

gaa gcc gcg gaa gct ttg atc gca gaa gtg cca gcg cca cgc gac aaa	96
Glu Ala Ala Glu Ala Leu Ile Ala Glu Val Pro Ala Pro Arg Asp Lys	
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gtc gag ctc atg gca ttt tcc aag tcc agg caa ggc cgc gtt gtc att	144
Val Glu Leu Met Ala Phe Ser Lys Ser Arg Gln Gly Arg Val Val Ile	
35 40 45	
gaa ctt gaa gac gcc aca gta gcc acc cct gat gat cgc atc ctg gta	192
Glu Leu Glu Asp Ala Thr Val Ala Thr Pro Asp Asp Arg Ile Leu Val	
50 55 60	
gaa gac ctc acc tgg cgt ttg gct cca gga gag cgc atc ggt ctt gtc	240
Glu Asp Leu Thr Trp Arg Leu Ala Pro Gly Glu Arg Ile Gly Leu Val	
65 70 75 80	
ggc gtc aac ggc tcc ggc aaa acc acc ctg ctg cgc acc ctt gcc ggc	288
Gly Val Asn Gly Ser Gly Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly	
85 90 95	
gag cag cca ctt cag gca ggc aaa cgc atc gaa ggc caa acc gtc aaa	336
Glu Gln Pro Leu Gln Ala Gly Lys Arg Ile Glu Gly Gln Thr Val Lys	
100 105 110	
ctg gga tgg ctc cgc cag gaa ctc gat gac cta gac ctc agc cgc cga	384
Leu Gly Trp Leu Arg Gln Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg	
115 120 125	
ctc atc gac tgc gtt gaa gat gtc gct tcc tac gtg atg atg ggc gac	432
Leu Ile Asp Cys Val Glu Asp Val Ala Ser Tyr Val Met Met Gly Asp	
130 135 140	
aag cag gtc tcc gct tcc caa ttg gca gaa cgc ctc gga ttc tca ccc	480
Lys Gln Val Ser Ala Ser Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro	
145 150 155 160	
aag agg caa cgc acc cca gtt ggt gac ctg tcc ggt ggt gaa cgc cgc	528
Lys Arg Gln Arg Thr Pro Val Gly Asp Leu Ser Gly Gly Glu Arg Arg	
165 170 175	
cga ctc caa ctc acc cgc gtg ctc atg gcc gaa cca aac gtg ctg ctc	576
Arg Leu Gln Leu Thr Arg Val Leu Met Ala Glu Pro Asn Val Leu Leu	
180 185 190	
ctc gac gag ccc acc aac gac ctg gac att gac acc ctc caa gag ctg	624
Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu	
195 200 205	
gaa tcc ctt ctc gac gga tgg cca ggc acc atg gtg gtt atc tcc cac	672
Glu Ser Leu Leu Asp Gly Trp Pro Gly Thr Met Val Val Ile Ser His	
210 215 220	
gac cgt tac ctc atc gaa cgc gtc acc gac tcc acc tgg gca ctc ttc	720
Asp Arg Tyr Leu Ile Glu Arg Val Thr Asp Ser Thr Trp Ala Leu Phe	
225 230 235 240	
ggc gat ggc aag ctc acc aac ctg cca ggc gga att gaa gag tac ctg	768
Gly Asp Gly Lys Leu Thr Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu	
245 250 255	

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Gln	Arg	Arg	Ala	Ala	Met	Ala	Ala	Ala	Glu	Asp	Ser	Gly	Val	Leu	Asn	
			260					265					270			
ttg	ggt	gcg	gcc	acg	cag	gct	gga	acc	ttt	tct	gct	gca	aca	gag	cag	864
Leu	Gly	Ala	Ala	Thr	Gln	Ala	Gly	Thr	Phe	Ser	Ala	Ala	Thr	Glu	Gln	
		275					280					285				
gct	gcc	act	tct	gtg	gaa	agt	tcc	gga	att	tct	tcc	caa	gaa	cgc	cac	912
Ala	Ala	Thr	Ser	Val	Glu	Ser	Ser	Gly	Ile	Ser	Ser	Gln	Glu	Arg	His	
		290				295					300					
cgc	atc	acc	aag	gaa	atg	aac	gcc	ctg	gag	cgc	aaa	atg	ggc	aag	ctt	960
Arg	Ile	Thr	Lys	Glu	Met	Asn	Ala	Leu	Glu	Arg	Lys	Met	Gly	Lys	Leu	
305					310					315					320	
gac	cag	caa	atg	gac	aag	ctt	aat	cag	cag	ctc	gct	gat	gca	gcg	gag	1008
Asp	Gln	Gln	Met	Asp	Lys	Leu	Asn	Gln	Gln	Leu	Ala	Asp	Ala	Ala	Glu	
				325					330					335		
gcc	atg	gac	acc	ata	aag	ctc	acc	gag	ctg	gac	acc	aag	ctc	cgc	gca	1056
Ala	Met	Asp		Thr	Ile	Lys	Leu	Thr	Glu	Leu	Asp	Thr	Lys	Leu	Arg	
				340					345					350	Ala	
gtg	cag	gaa	gaa	cac	ggc	gag	ctg	gaa	atg	cag	tgg	ctg	gaa	ctc	ggc	1104
Val	Gln	Glu	Glu	His	Gly	Glu	Leu	Glu	Met	Gln	Trp	Leu	Glu	Leu	Gly	
		355					360						365			
gag	gaa	atc	gag	ggc	tagttcatgc	cgtcggcagg	cga									1142
Glu	Glu	Ile	Glu	Gly												
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Glu	Ala	Ala	Glu	Ala	Leu	Ile	Ala	Glu	Val	Pro	Ala	Pro	Arg	Asp	Lys	
			20					25					30			
Val	Glu	Leu	Met	Ala	Phe	Ser	Lys	Ser	Arg	Gln	Gly	Arg	Val	Val	Ile	
		35					40					45				
Glu	Leu	Glu	Asp	Ala	Thr	Val	Ala	Thr	Pro	Asp	Asp	Arg	Ile	Leu	Val	
	50					55					60					
Glu	Asp	Leu	Thr	Trp	Arg	Leu	Ala	Pro	Gly	Glu	Arg	Ile	Gly	Leu	Val	
65					70					75					80	
Gly	Val	Asn	Gly	Ser	Gly	Lys	Thr	Thr	Leu	Leu	Arg	Thr	Leu	Ala	Gly	
				85					90					95		
Glu	Gln	Pro	Leu	Gln	Ala	Gly	Lys	Arg	Ile	Glu	Gly					

115	120	125
Leu Ile Asp Cys Val Glu Asp Val Ala Ser Tyr Val Met Met Gly Asp 130	135	140
Lys Gln Val Ser Ala Ser Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro 145	150	155 160
Lys Arg Gln Arg Thr Pro Val Gly Asp Leu Ser Gly Gly Glu Arg Arg 165	170	175
Arg Leu Gln Leu Thr Arg Val Leu Met Ala Glu Pro Asn Val Leu Leu 180	185	190
Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu 195	200	205
Glu Ser Leu Leu Asp Gly Trp Pro Gly Thr Met Val Val Ile Ser His 210	215	220
Asp Arg Tyr Leu Ile Glu Arg Val Thr Asp Ser Thr Trp Ala Leu Phe 225	230	235 240
Gly Asp Gly Lys Leu Thr Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu 245	250	255
Gln Arg Arg Ala Ala Met Ala Ala Ala Glu Asp Ser Gly Val Leu Asn 260	265	270
Leu Gly Ala Ala Thr Gln Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln 275	280	285
Ala Ala Thr Ser Val Glu Ser Ser Gly Ile Ser Ser Gln Glu Arg His 290	295	300
Arg Ile Thr Lys Glu Met Asn Ala Leu Glu Arg Lys Met Gly Lys Leu 305	310	315 320
Asp Gln Gln Met Asp Lys Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu 325	330	335
Ala Met Asp Thr Ile Lys Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala 340	345	350
Val Gln Glu Glu His Gly Glu Leu Glu Met Gln Trp Leu Glu Leu Gly 355	360	365
Glu Glu Ile Glu Gly 370		

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<211> 349

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(349)

<223> RXN02975

<222> (101) . . (709)

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gtc gaa aag cat ttt gct ttt ggt ctt aaa gct gcg aag cag cgt cgc 163
Val Glu Lys His Phe Ala Phe Gly Leu Lys Ala Ala Lys Gln Arg Arg
10 15 20

gca ggt ctg agc gtt ttt gat tat gtg ctg ctg ggg cgt cat ccg cac 259
Ala Gly Leu Ser Val Phe Asp Tyr Val Leu Leu Gly Arg His Pro His
40 45 50

gct gat ctg aaa ttg gag cat ttc agc gac cgc ggc tta gac gaa ttg 355
Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg Gly Leu Asp Glu Leu
70 75 80 85

gaa ccg cgc atc gtg ctt ctc gac gag ccg acc tcc gcg ctt gac atc 451
Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Ile
105 110 115

ctc ggc ctc acc gtg atc gcg gcg atg cat gac ctc acc ctg act gcg 547
Leu Gly Leu Thr Val Ile Ala Ala Met His Asp Leu Thr Leu Thr Ala
135 140 145

caa tac ggc gat cgg gtg ctc atg atg aat ggt ggc cgc aaa gtt ttc 595
Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly Gly Arg Lys Val Phe
150 155 160 165

gag ggc act gca gcc gaa gtg ctc acc gcg cag cgg att tcg gag att 643
Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln Arg Ile Ser Glu Ile
170 175 180

tat	gat	gcc	act	gtg	att	gtt	gag	gtt	att	gat	ggg	cgt	ccc	gtg	gtg	691
Tyr	Asp	Ala	Thr	Val	Ile	Val	Glu	Val	Ile	Asp	Gly	Arg	Pro	Val	Val	
			185				190					195				

att ccg caa cgg tcg cac tgacctgttg tggcagacca gac 732
Ile Pro Gln Arg Ser His
200

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 <213> Corynebacterium glutamicum

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 35 40 45
 Gly Arg His Pro His Ser Tyr Ala Pro Gly Arg Ala Asp Asp Glu Ile
 50 55 60
 Val Lys Arg Cys Leu Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg
 65 70 75 80
 Gly Leu Asp Glu Leu Ser Gly Gly Glu Arg Gln Arg Val Ser Leu Ala
 85 90 95
 Arg Ala Leu Ala Gln Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr
 100 105 110
 Ser Ala Leu Asp Ile Gly His Ala Gln Glu Thr Leu Glu Leu Ile Asp
 115 120 125
 Ala Ile Arg His Arg Leu Gly Leu Thr Val Ile Ala Ala Met His Asp
 130 135 140
 Leu Thr Leu Thr Ala Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly
 145 150 155 160
 Gly Arg Lys Val Phe Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln
 165 170 175
 Arg Ile Ser Glu Ile Tyr Asp Ala Thr Val Ile Val Glu Val Ile Asp
 180 185 190
 Gly Arg Pro Val Val Ile Pro Gln Arg Ser His
 195 200

<210> 161
 <211> 390
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(367)
 <223> RXN03108

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	Met	Thr	Lys	Pro	Asn	
	1				5	
gct tcc gtc gag ctg aat acg atc acc aag tcc tac ggc tcc acc act						163
Ala Ser Val Glu Leu Asn Thr Ile Thr Lys Ser Tyr Gly Ser Thr Thr						
				10	15	20
atc att ggc gat acg agc atc acc atc aac gac ggt gaa ttc gtc tcc						211
Ile Ile Gly Asp Thr Ser Ile Thr Ile Asn Asp Gly Glu Phe Val Ser						
				25	30	35
ctc ctc gac cct tcc ggc tgc gga aaa tca aca att ctc aaa atg atc						259
Leu Leu Asp Pro Ser Gly Cys Gly Lys Ser Thr Ile Leu Lys Met Ile						
				40	45	50
gcc gga ctg gcc tcc cca tcc acc ggc aca gtc agc gca ggc aac gaa						307
Ala Gly Leu Ala Ser Pro Ser Thr Gly Thr Val Ser Ala Gly Asn Glu						
				55	60	65
gaa att aaa gga cca gga cct gac cga ggc atg gtt ttc caa gac cac						355
Glu Ile Lys Gly Pro Gly Pro Asp Arg Gly Met Val Phe Gln Asp His						
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gcc ctc ctg ccc tgattgaccg cacgcggcaa cat						390
Ala Leu Leu Pro						

<210> 162
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 <212> PRT
 <213> Corynebacterium glutamicum

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 Gly Glu Phe Val Ser Leu Leu Asp Pro Ser Gly Cys Gly Lys Ser Thr
 35 40 45
 Ile Leu Lys Met Ile Ala Gly Leu Ala Ser Pro Ser Thr Gly Thr Val
 50 55 60
 Ser Ala Gly Asn Glu Glu Ile Lys Gly Pro Gly Pro Asp Arg Gly Met
 65 70 75 80
 Val Phe Gln Asp His Ala Leu Leu Pro
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<210> 163
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 <213> Corynebacterium glutamicum

<220>
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 215 220 225

gcg ttc gtc gcc agc ttc att ggt tcc cct tcc atg aac ttg att gag 835
 Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser Met Asn Leu Ile Glu
 230 235 240 245

ggc acc atc cgt ggc gat aag gtc act ttg ggt act gga att cag att 883
 Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly Thr Gly Ile Gln Ile
 250 255 260

tca gtt cct gat gag gtg gca gca gag gtt cgc aac aac ccg gat cgc 931
 Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg Asn Asn Pro Asp Arg
 265 270 275

ttt gag ggt cgt cca gtc att gtt ggt gct cgt ccc gag cac atg tat 979
 Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg Pro Glu His Met Tyr
 280 285 290

ttg acc acg gcg aat gag agt ggt gct gta ttg ggc gaa gtc agc cac 1027
 Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu Gly Glu Val Ser His
 295 300 305

att gat gag ctc ggc gcg gat tca atg gtc tac gta ttg gcg tct ggt 1075
 Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr Val Leu Ala Ser Gly
 310 315 320 325

gtg aag aac ccg aat act gat ctt ttg ggt gag ggc att cca gag gat 1123
 Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu Gly Ile Pro Glu Asp
 330 335 340

atg cgc gtg acc gtt gtc ggt gct gaa gag acc gat aag gcc cgg ctg 1171
 Met Arg Val Thr Val Val Gly Ala Glu Glu Thr Asp Lys Ala Arg Leu
 345 350 355

ggt att cgt gtt gag cgc cat cac ggt ctg aag gcc ggc gat aag gtg 1219
 Gly Ile Arg Val Glu Arg His His Gly Leu Lys Ala Gly Asp Lys Val
 360 365 370

cac gtt gtt gct gca ccg aag gat gtt cac ctc ttc gac ggt ctt gat 1267
 His Val Val Ala Ala Pro Lys Asp Val His Leu Phe Asp Gly Leu Asp
 375 380 385

ggc cgt cga atc ggt gca tcg gtt cta gct cca gcc cat aca gtc cag 1315
 Gly Arg Arg Ile Gly Ala Ser Val Leu Ala Pro Ala His Thr Val Gln
 390 395 400 405

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 Ser Gly His

<210> 164

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

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 20 25 30
 Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu
 35 40 45
 Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile
 50 55 60
 Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala
 65 70 75 80
 Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp
 85 90 95
 Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile
 100 105 110
 Glu Lys Arg Val Ala Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr
 115 120 125
 Leu Asp Arg Lys Pro Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
 130 135 140
 Ala Met Gly Arg Ala Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp
 145 150 155 160
 Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala
 165 170 175
 Glu Ile Ser Gly Leu Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val
 180 185 190
 Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
 195 200 205
 Leu Leu Leu Gly Val Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr
 210 215 220
 Asp Tyr Pro Ala Asn Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser
 225 230 235 240
 Met Asn Leu Ile Glu Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly
 245 250 255
 Thr Gly Ile Gln Ile Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg
 260 265 270
 Asn Asn Pro Asp Arg Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg
 275 280 285
 Pro Glu His Met Tyr Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu
 290 295 300
 Gly Glu Val Ser His Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr
 305 310 315 320
 Val Leu Ala Ser Gly Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu
 325 330 335

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Gly Ile Pro Glu Asp Met Arg Val Thr Val Val Gly Ala Glu Glu Thr
 340 345 350

Asp Lys Ala Arg Leu Gly Ile Arg Val Glu Arg His His Gly Leu Lys
 355 360 365

Ala Gly Asp Lys Val His Val Val Ala Ala Pro Lys Asp Val His Leu
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Phe Asp Gly Leu Asp Gly Arg Arg Ile Gly Ala Ser Val Leu Ala Pro
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Ala His Thr Val Gln Ser Gly His
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 <223> FRXA01890

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 Met Ala Ser Ile Val
 1 5

ttt gaa aac gtc aca cgc aaa tac tct ccg ggc gca cgc ccg gcc gtc 163
 Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly Ala Arg Pro Ala Val
 10 15 20

gac aag ctt aat ttg gaa atc gcc gac ggc gag ttc cta gtt ctc gtt 211
 Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
 25 30 35

gga ccc tca ggc tgt gga aag tcc act tct ttg cgc atg ctg gct ggt 259
 Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu Arg Met Leu Ala Gly
 40 45 50

ctt gag cct atc gac gag gga cgt cta ctc att gat ggt aaa gac gcc 307
 Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile Asp Gly Lys Asp Ala
 55 60 65

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 Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala Met Val Phe Gln Ser
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 Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp Asn Met Gly Phe Ala
 90 95 100

ctg aag aat cag aag gtg gct aag gct gag atc gaa aag cgt gtt gct 451
 Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile Glu Lys Arg Val Ala
 105 110 115

gaa gcc tca cgc att ctg cag ctg gat ccg tat ctt gat cgt aag cct 499
 Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr Leu Asp Arg Lys Pro
 120 125 130

gca gct ttg tct ggt ggt cag cgc cag cgc gtg gcc atg ggc cgt gca 547
 Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
 135 140 145

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 Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp Glu Pro Leu Ser Asn
 150 155 160 165

cta gat gcg aag ctg cgt gtg tct acg cgt gcg gag atc tct ggt ttg 643
 Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala Glu Ile Ser Gly Leu
 170 175 180

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 Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Val
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gag gcc atg acc atg ggt gat cgc gtc gct gtg ctt ttg ctc ggt gtg 739
 Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Leu Leu Gly Val
 200 205 210

ctg cag caa gta gac acc ccg cag aac ctg tac gac tac cca gca aat 787
 Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr Asp Tyr Pro Ala Asn
 215 220 225

gcg ttc gtc gcc agc ttc att ggt tcc ctt cca tgaacttgat tgagggcacc 840
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atc 843

<210> 166

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

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 35 40 45

Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile
 50 55 60

Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala
 65 70 75 80

Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp
 85 90 95

Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile
 100 105 110

Asp Tyr Pro Ala Asn Ala Phe Val Ala Ser Phe Ile Gly Ser Leu Pro
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Met Thr Thr Ala Leu
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Gly Thr Arg Val Val Ala Arg Asn Phe Gly Tyr Arg His Ala Ser Arg
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gaa aac ccc gcg ctc aaa gac atc aac ttc gag atc gca cct ggt gaa 211
Glu Asn Pro Ala Leu Lys Asp Ile Asn Phe Glu Ile Ala Pro Gly Glu
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Arg Ile Leu Leu Thr Gly Ala Ser Gly Ala Gly Lys Ser Thr Leu Leu
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Ala Ala Leu Ala Gly Val Leu Gly Gly Ser Asp Glu Gly Val Ser Thr
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cca gat tcc caa gtc atc gcc tcc cgc atc ggc gat gat gtg gcg ttt	403
Pro Asp Ser Gln Val Ile Ala Ser Arg Ile Gly Asp Asp Val Ala Phe	
90 95 100	
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Gly Cys Glu Asn Leu Gln Ile Pro Arg Glu Glu Ile Trp Pro Arg Val	
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Glu Arg Ala Leu Glu Leu Val Gly Leu Asp Leu Pro Leu Ser His Pro	
120 125 130	
acg aaa tat ctt tcc ggt ggc caa aaa caa cgc ctc gct ctt gcc ggt	547
Thr Lys Tyr Leu Ser Gly Gly Gln Lys Gln Arg Leu Ala Leu Ala Gly	
135 140 145	
gtg atc gcc atg ggt gct cgt ctg att ctg ctt gat gaa ccc acc gca	595
Val Ile Ala Met Gly Ala Arg Leu Ile Leu Leu Asp Glu Pro Thr Ala	
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Asn Leu Asp Pro Gln Gly Gln Lys Asn Val Val Ala Ala Val Asp Arg	
170 175 180	
gtt gtt cag gaa act gga gca aca ctc atc gtg gtg gaa cac cgc cat	691
Val Val Gln Glu Thr Gly Ala Thr Leu Ile Val Val Glu His Arg His	
185 190 195	
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Glu Leu Trp Val Asn Ile Ile Asp Arg Ile Ile Ser Ile Thr Asp Gly	
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Ala Gln Pro Ser Thr Ser Lys Pro Ile Leu Trp Ala Asn Asp Leu Leu	
230 235 240 245	
tgc acc tgg ggc ggc ctg cgt agt ttt gag gtg ccg gaa ggc gcc tcg	883
Cys Thr Trp Gly Gly Leu Arg Ser Phe Glu Val Pro Glu Gly Ala Ser	
250 255 260	
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Thr Val Ile Thr Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Ala Leu	
265 270 275	
acc atg ggt gga ttg ctt ccg cga aaa gtg ggc agc tgg aac tct ctg	979
Thr Met Gly Gly Leu Leu Pro Arg Lys Val Gly Ser Trp Asn Ser Leu	
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aca cgg tgc gcg gcg gcc tta aca cgc ccc cgc aca agt ggc gtt cag	1027
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1056

<400> 168																
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Ile	Ala	Pro	Gly	Glu	Arg	Ile	Leu	Leu	Thr	Gly	Ala	Ser	Gly	Ala	Gly	
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Lys	Ser	Thr	Leu	Leu	Ala	Ala	Leu	Ala	Gly	Val	Leu	Gly	Gly	Ser	Asp	
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Glu	Gly	Val	Ser	Thr	Gly	Glu	Leu	Leu	Val	Asp	Ala	Pro	Ser	Ile	Gly	
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Asp	Asp	Val	Ala	Phe	Gly	Cys	Glu	Asn	Leu	Gln	Ile	Pro	Arg	Glu	Glu	
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Ile	Trp	Pro	Arg	Val	Glu	Arg	Ala	Leu	Glu	Leu	Val	Gly	Leu	Asp	Leu	
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Pro	Leu	Ser	His	Pro	Thr	Lys	Tyr	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	
	130					135					140					
Leu	Ala	Leu	Ala	Gly	Val	Ile	Ala	Met	Gly	Ala	Arg	Leu	Ile	Leu	Leu	
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Asp	Glu	Pro	Thr	Ala	Asn	Leu	Asp	Pro	Gln	Gly	Gln	Lys	Asn	Val	Val	
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Ala	Ala	Val	Asp	Arg	Val	Val	Gln	Glu	Thr	Gly	Ala	Thr	Leu	Ile	Val	
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Val	Glu	His	Arg	His	Glu	Leu	Trp	Val	Asn	Ile	Ile	Asp	Arg	Ile	Ile	
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Ser	Ile	Thr	Asp	Gly	Glu	Asp	Val	Gln	Pro	Ala	Glu	Leu	Ile	Lys	Val	
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Gly	Gln	Leu	Pro	Gly	Ala	Gln	Pro	Ser	Thr	Ser	Lys	Pro	Ile	Leu	Trp	
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Ala	Asn	Asp	Leu	Leu	Cys	Thr	Trp	Gly	Gly	Leu	Arg	Ser	Phe	Glu	Val	
				245					250					255		
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Tyr	Leu	Val	Ser	Phe	Gln	Ile	Val	Gln	Ala	Leu	Ala	Pro	Thr	Leu	Ala	
	135					140					145					
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Val	Ser	Leu	Gly	Ser	Trp	Ala	Leu	Leu	Gly	Leu	Val	Ala	Ala	Ile	Ser	
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Trp	Ile	Pro	Leu	Leu	Ser	Leu	Gln	Gly	Ala	Arg	Val	Val	Ala	Ala	Pro	
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tcg	aag	gtt	tct	ctt	cct	gtg	tgg	aag	tct	tcg	gtt	ggg	gtg	ggg	ctc	739
Ser	Lys	Val	Ser	Leu	Pro	Val	Trp	Lys	Ser	Ser	Val	Gly	Val	Gly	Leu	
	200						205					210				
ggg	ttg	atg	ttt	ggg	ttt	act	tcg	ttt	gcg	acg	tat	atc	ctc	atg	ggg	787
Gly	Leu	Met	Phe	Gly	Phe	Thr	Ser	Phe	Ala	Thr	Tyr	Ile	Leu	Met	Gly	
215						220					225					
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Phe	Met	Pro	Gln	Met	Val	Gly	Asp	Pro	Gln	Leu	Gly	Ala	Val	Leu	Leu	
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Gly	Trp	Trp	Ser	Ile	Leu	Gly	Leu	Pro	Leu	Asn	Ile	Leu	Gly	Pro	Trp	
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Leu	Val	Thr	Arg	Phe	Thr	Asn	Cys	Phe	Pro	Met	Val	Val	Ile	Ala	Ser	
			265					270					275			
gtc	atg	ttt	ctc	atc	ggg	aat	ggg	ggg	ttt	tgt	ttg	gct	ccg	gat	gtt	979
Val	Met	Phe	Leu	Ile	Gly	Asn	Gly	Gly	Phe	Cys	Leu	Ala	Pro	Asp	Val	
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gcg	ccg	tgg	ttg	tgg	gcg	acg	ttg	tct	ggg	ctt	ggg	ccc	ctt	gcg	ttc	1027
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ccg	atg	gcg	ttg	acg	ctc	att	aat	att	cgt	gct	gaa	act	agt	gct	ggg	1075
Pro	Met	Ala	Leu	Thr	Leu	Ile	Asn	Ile	Arg	Ala	Glu	Thr	Ser	Ala	Gly	
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Ala	Ser	Ala	Leu	Ser	Ser	Phe	Gly	Gln	Gly	Leu	Gly	Tyr	Thr	Ile	Ala	
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tgt	ttc	ggg	ccc	ttg	ttg	act	ggg	ttc	att	gtc	gat	gcg	aca	ggc	agc	1171
Cys	Phe	Gly	Pro	Leu	Leu	Thr	Gly	Phe	Ile	Val	Asp	Ala	Thr	Gly	Ser	
			345					350					355			
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Phe	Arg	Thr	Ile	Phe	Val	Leu	Phe	Ala	Val	Ala	Thr	Leu	Phe	Val	Ile	
	360						365					370				
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1296

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Leu Thr Gly Trp Arg Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu
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 Val Ala Ala Ile Ser Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg
 180 185 190
 Val Val Ala Ala Pro Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser
 195 200 205
 Val Gly Val Gly Leu Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr
 210 215 220
 Tyr Ile Leu Met Gly Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu
 225 230 235 240
 Gly Ala Val Leu Leu Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn
 245 250 255
 Ile Leu Gly Pro Trp Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met
 260 265 270
 Val Val Ile Ala Ser Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys
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 Leu Ala Pro Asp Val Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu
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 Gly Pro Leu Ala Phe Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala
 305 310 315 320
 Glu Thr Ser Ala Gly Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu
 325 330 335
 Gly Tyr Thr Ile Ala Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val
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 Asp Ala Thr Gly Ser Phe Arg Thr Ile Phe Leu Leu Phe Ala Gly Ala
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<222> (101)..(1483)

<223> RXA00634

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 Met Trp Glu Arg Phe

tgg ctc att atc cag ccc tta cga cac cca caa gtc agc tcc gaa gag 883
 Trp Leu Ile Ile Gln Pro Leu Arg His Pro Gln Val Ser Ser Glu Glu
 250 255 260

aaa cga aaa gtg ctg gca ttc atc ccg atc ttc gtc tgc tca acc gca 931
 Lys Arg Lys Val Leu Ala Phe Ile Pro Ile Phe Val Cys Ser Thr Ala
 265 270 275

ttc tgg gca gtg caa gca caa acc tac ggc gta cta gct gtg tac tcc 979
 Phe Trp Ala Val Gln Ala Gln Thr Tyr Gly Val Leu Ala Val Tyr Ser
 280 285 290

caa gaa cgt gtt gac cgc atg gtt ggc gat ttt gag atc cca gca gcc 1027
 Gln Glu Arg Val Asp Arg Met Val Gly Asp Phe Glu Ile Pro Ala Ala
 295 300 305

tgg tca caa tca ctc aat cct ttt ttc atc ctg gcg ctg tcc atc ccg 1075
 Trp Ser Gln Ser Leu Asn Pro Phe Phe Ile Leu Ala Leu Ser Ile Pro
 310 315 320 325

att tcc ctg tgg ttt atg cgc gga tca cgc gcc cca aga gtg aaa att 1123
 Ile Ser Leu Trp Phe Met Arg Gly Ser Arg Ala Pro Arg Val Lys Ile
 330 335 340

gga atc agc att gga gtg atc att gcg gga agt ggg ctt cta gtt ctt 1171
 Gly Ile Ser Ile Gly Val Ile Ile Ala Gly Ser Gly Leu Leu Val Leu
 345 350 355

att cca ttt gtt gga atg ccg ctc gcg cca gtg tgg gtg ctg cct tta 1219
 Ile Pro Phe Val Gly Met Pro Leu Ala Pro Val Trp Val Leu Pro Leu
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agt gtt ttc ctc atc tca ctg gga gaa ctt ttc atc gga ccc gga gga 1267
 Ser Val Phe Leu Ile Ser Leu Gly Glu Leu Phe Ile Gly Pro Gly Gly
 375 380 385

atg gct gcg act gcg cac cac gca cca cga ata ttt gcc aca cga ttc 1315
 Met Ala Ala Thr Ala His His Ala Pro Arg Ile Phe Ala Thr Arg Phe
 390 395 400 405

tcc gcc ctg tat ttc ctc aca ctc gcc atc ggc atg tct att gca ggt 1363
 Ser Ala Leu Tyr Phe Leu Thr Leu Ala Ile Gly Met Ser Ile Ala Gly
 410 415 420

aat gtg tcc aaa ttt tac gac ccc acc aac cac acc tcc gag ctc cga 1411
 Asn Val Ser Lys Phe Tyr Asp Pro Thr Asn His Thr Ser Glu Leu Arg
 425 430 435

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 Tyr Phe Ala Val Phe Gly Ile Ser Ile Ile Val Ile Gly Val Gly Ser
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<211> 461

<212> PRT

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 35 40 45
 Cys Trp Ala Gly Gly Trp Val Ser Asp Arg Val Leu Gly Ala Glu Lys
 50 55 60
 Thr Leu Leu Gly Gly Ala Ile Ser Val Thr Ile Gly His Leu Val Leu
 65 70 75 80
 Ala Gly Leu Gly Gly Lys Ile Gly Leu Ala Ile Gly Leu Gly Cys Ile
 85 90 95
 Ala Ile Gly Ser Gly Phe Val Lys Thr Ala Ala Ile Thr Val Leu Gly
 100 105 110
 Ser Arg His Gly Glu Gln Glu Gly Asp Ala Lys Ala Asp Pro Ala Phe
 115 120 125
 Gln Leu Phe Tyr Leu Gly Ile Asn Val Gly Ala Leu Leu Gly Pro Leu
 130 135 140
 Leu Thr Gly Trp Leu Ser Ser Arg Tyr Ser Phe Glu Met Gly Phe Gly
 145 150 155 160
 Ala Ala Ala Val Leu Met Ile Gly Gly Leu Gly Ile Tyr Ala Ala Leu
 165 170 175
 Arg Lys Pro Met Leu Gln Ser Phe Pro Leu Glu Val Lys Lys Ala Leu
 180 185 190
 Leu Arg Ala Gln Asn Pro Ala Glu Lys His Val Ile Ser Thr Ala Phe
 195 200 205
 Ala Ala Val Ala Val Leu Cys Gly Val Leu Leu Tyr Leu Leu Leu Thr
 210 215 220
 Glu Thr Val Ser Ala Asp Gln Leu Ala Gly Ala Leu Leu Leu Val Thr
 225 230 235 240
 Ile Gly Ala Ala Leu Trp Leu Ile Ile Gln Pro Leu Arg His Pro Gln
 245 250 255
 Val Ser Ser Glu Glu Lys Arg Lys Val Leu Ala Phe Ile Pro Ile Phe
 260 265 270
 Val Cys Ser Thr Ala Phe Trp Ala Val Gln Ala Gln Thr Tyr Gly Val
 275 280 285
 Leu Ala Val Tyr Ser Gln Glu Arg Val Asp Arg Met Val Gly Asp Phe
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Pro Arg Val Lys	Ile Gly Ile Ser Ile Gly Val Ile Ile Ala Gly Ser					
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Gly Leu Leu Val	Leu Ile Pro Phe Val Gly Met Pro Leu Ala Pro Val					
	355			360		365
Trp Val Leu Pro	Leu Ser Val Phe Leu Ile Ser Leu Gly Glu Leu Phe					
	370			375		380
Ile Gly Pro Gly	Gly Met Ala Ala Thr Ala His His Ala Pro Arg Ile					
	385			390		395
Phe Ala Thr Arg	Phe Ser Ala Leu Tyr Phe Leu Thr Leu Ala Ile Gly					
	405			410		415
Met Ser Ile Ala	Gly Asn Val Ser Lys Phe Tyr Asp Pro Thr Asn His					
	420			425		430
Thr Ser Glu Leu	Arg Tyr Phe Ala Val Phe Gly Ile Ser Ile Ile Val					
	435			440		445
Ile Gly Val Gly	Ser Leu Met Val Ala Lys Lys Val Gly					
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1624)
 <223> RXA02451

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 Met Asn Thr Asp Thr
 1 5
 act caa gac ggt gtg agt cct gaa cct tcc gac ccc cac cta ggg tct 163
 Thr Gln Asp Gly Val Ser Pro Glu Pro Ser Asp Pro His Leu Gly Ser
 10 15 20
 gaa gtg gcg gaa act cac cgc gaa aag aaa ttc ttc ggc cag cct tgg 211
 Glu Val Ala Glu Thr His Arg Glu Lys Lys Phe Phe Gly Gln Pro Trp
 25 30 35
 ggg ctg gca aat ctc ttc ggc gtg gag atg tgg gag cga ttc agc ttc 259
 Gly Leu Ala Asn Leu Phe Gly Val Glu Met Trp Glu Arg Phe Ser Phe
 40 45 50
 tac ggc atg cag tcc atc ctt gct ttc tat ctg tac tac tcc gtc acc 307
 Tyr Gly Met Gln Ser Ile Leu Ala Phe Tyr Leu Tyr Tyr Ser Val Thr

55	60	65	
gat ggc gga ctt ggt atg aat cag aca gct gca ctg tcc att gtg ggc Asp Gly Gly Leu Gly Met Asn Gln Thr Ala Ala Leu Ser Ile Val Gly 70 75 80 85			355
gcc tac ggc ggc ttc gtc tac atg acc tcc ctc gtg gct tcc ttc att Ala Tyr Gly Gly Phe Val Tyr Met Thr Ser Leu Val Ala Ser Phe Ile 90 95 100			403
gca gac cga gta ttg ggc tct gaa cgt aca ctc ttc tac tcc gcg atc Ala Asp Arg Val Leu Gly Ser Glu Arg Thr Leu Phe Tyr Ser Ala Ile 105 110 115			451
atc gtc atg ctg ggc cac att gcc ctg gcc ttg att ccg gga tat acg Ile Val Met Leu Gly His Ile Ala Leu Ala Leu Ile Pro Gly Tyr Thr 120 125 130			499
gga ctg tcc atc ggc ttg gtc ctc atc ggc ctt ggc tca ggt ggc gtg Gly Leu Ser Ile Gly Leu Val Leu Ile Gly Leu Gly Ser Gly Gly Val 135 140 145			547
aag acg gca gcg cag gtt gtg ctg ggc cag ctg tac tca cgc acg gac Lys Thr Ala Ala Gln Val Val Leu Gly Gln Leu Tyr Ser Arg Thr Asp 150 155 160 165			595
acg cgt cga gac gca ggc ttc tcc atc ttc tac atg ggc gtc aac ctc Thr Arg Arg Asp Ala Gly Phe Ser Ile Phe Tyr Met Gly Val Asn Leu 170 175 180			643
ggt ggc ctc ttt ggc ccg ctg atc acc aac gct ctg tgg gga tgg gga Gly Gly Leu Phe Gly Pro Leu Ile Thr Asn Ala Leu Trp Gly Trp Gly 185 190 195			691
gga ttc cac tgg ggc ttc ggt atc gcc gca gtc ggc atg gct ttg ggt Gly Phe His Trp Gly Phe Gly Ile Ala Ala Val Gly Met Ala Leu Gly 200 205 210			739
ctc atc caa tac gtg gcg atg cgt aaa acc acc atc ggt gcg gca ggc Leu Ile Gln Tyr Val Ala Met Arg Lys Thr Thr Ile Gly Ala Ala Gly 215 220 225			787
cat act gtt cct aac cca ctg cct aag aat gaa tat gcg cgc tgg att His Thr Val Pro Asn Pro Leu Pro Lys Asn Glu Tyr Ala Arg Trp Ile 230 235 240 245			835
atc ggt gca gtc gtg gtt gtc gca gca gtt gtc gct ctc atc gca acg Ile Gly Ala Val Val Val Val Ala Ala Val Val Ala Leu Ile Ala Thr 250 255 260			883
ggc atc atc aag ctg gaa tgg ctg tcc aac atc acc gca gcg atc gca Gly Ile Ile Lys Leu Glu Trp Leu Ser Asn Ile Thr Ala Ala Ile Ala 265 270 275			931
ctg att gcg gct att gct ctg ctt gct cag atg tac gtt tcc cca ctg Leu Ile Ala Ala Ile Ala Leu Leu Ala Gln Met Tyr Val Ser Pro Leu 280 285 290			979
acc acc gca gcg gaa aag tcc cgc ttg ttg gga ttc atc ccg atg ttc Thr Thr Ala Ala Glu Lys Ser Arg Leu Leu Gly Phe Ile Pro Met Phe 295 300 305			1027

atc ggt ggc gtg ctt ttc ttc gcg atc ttc caa acc cag ttc acg gtc 1075
 Ile Gly Gly Val Leu Phe Phe Ala Ile Phe Gln Thr Gln Phe Thr Val
 310 315 320 325

ctc gcg gtt tac tcc gac acc cgc ctg gac cgt aac ttc ttc ggc att 1123
 Leu Ala Val Tyr Ser Asp Thr Arg Leu Asp Arg Asn Phe Phe Gly Ile
 330 335 340

gat ctt cct cca gga ttg atc aac tcc ttc aac cca atc ttc atc atc 1171
 Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn Pro Ile Phe Ile Ile
 345 350 355

atc ttc tcc gga atc ttt gcc acc ttg tgg aca aaa ctc gga gca aag 1219
 Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr Lys Leu Gly Ala Lys
 360 365 370

cag tgg tct act gca gtg aag ttc ggt gtc gcc aac att gtc att ggt 1267
 Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala Asn Ile Val Ile Gly
 375 380 385

tgc gcg ctg ttc ttc ttc ctg ccg ttc gcc ggc ggt gca gag aac tct 1315
 Cys Ala Leu Phe Phe Phe Leu Pro Phe Ala Gly Gly Ala Glu Asn Ser
 390 395 400 405

acc cca atg gca ctg atc att tgg gtc tac ttc ctc ttc acc atc gct 1363
 Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe Leu Phe Thr Ile Ala
 410 415 420

gag ctt ctg ctc tcc cct gtc ggc aac tca ctt gca acc aag gtc gca 1411
 Glu Leu Leu Leu Ser Pro Val Gly Asn Ser Leu Ala Thr Lys Val Ala
 425 430 435

ccc gag gca ttc cag tcc cgc atg ttc gcc gtg tgg ctg atg gct gtc 1459
 Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val Trp Leu Met Ala Val
 440 445 450

tcc atg ggt acg tcc ctg tcc gcc acc ctg ggt ggt tac tac gat cca 1507
 Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly Gly Tyr Tyr Asp Pro
 455 460 465

acc gat gca gga tct gaa aag gtc ttc ttc att acc gtt ggc gtt gca 1555
 Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile Thr Val Gly Val Ala
 470 475 480 485

gcc atc gtt ctt ggt gca atc gtc ata gca gcc aag ggc tgg gtg ctg 1603
 Ala Ile Val Leu Gly Ala Ile Val Ile Ala Ala Lys Gly Trp Val Leu
 490 495 500

aag aag ttc atc gac gtc cga taggcctcac aaagcctcaa aac 1647
 Lys Lys Phe Ile Asp Val Arg
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<210> 178

<211> 508

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Met Asn Thr Asp Thr Thr Gln Asp Gly Val Ser Pro Glu Pro Ser Asp

1	5	10	15
Pro His Leu Gly Ser Glu Val Ala Glu Thr His Arg Glu Lys Lys Phe	20	25	30
Phe Gly Gln Pro Trp Gly Leu Ala Asn Leu Phe Gly Val Glu Met Trp	35	40	45
Glu Arg Phe Ser Phe Tyr Gly Met Gln Ser Ile Leu Ala Phe Tyr Leu	50	55	60
Tyr Tyr Ser Val Thr Asp Gly Gly Leu Gly Met Asn Gln Thr Ala Ala	65	70	75
Leu Ser Ile Val Gly Ala Tyr Gly Gly Phe Val Tyr Met Thr Ser Leu	85	90	95
Val Ala Ser Phe Ile Ala Asp Arg Val Leu Gly Ser Glu Arg Thr Leu	100	105	110
Phe Tyr Ser Ala Ile Ile Val Met Leu Gly His Ile Ala Leu Ala Leu	115	120	125
Ile Pro Gly Tyr Thr Gly Leu Ser Ile Gly Leu Val Leu Ile Gly Leu	130	135	140
Gly Ser Gly Gly Val Lys Thr Ala Ala Gln Val Val Leu Gly Gln Leu	145	150	155
Tyr Ser Arg Thr Asp Thr Arg Arg Asp Ala Gly Phe Ser Ile Phe Tyr	165	170	175
Met Gly Val Asn Leu Gly Gly Leu Phe Gly Pro Leu Ile Thr Asn Ala	180	185	190
Leu Trp Gly Trp Gly Gly Phe His Trp Gly Phe Gly Ile Ala Ala Val	195	200	205
Gly Met Ala Leu Gly Leu Ile Gln Tyr Val Ala Met Arg Lys Thr Thr	210	215	220
Ile Gly Ala Ala Gly His Thr Val Pro Asn Pro Leu Pro Lys Asn Glu	225	230	235
Tyr Ala Arg Trp Ile Ile Gly Ala Val Val Val Val Ala Ala Val Val	245	250	255
Ala Leu Ile Ala Thr Gly Ile Ile Lys Leu Glu Trp Leu Ser Asn Ile	260	265	270
Thr Ala Ala Ile Ala Leu Ile Ala Ala Ile Ala Leu Leu Ala Gln Met	275	280	285
Tyr Val Ser Pro Leu Thr Thr Ala Ala Glu Lys Ser Arg Leu Leu Gly	290	295	300
Phe Ile Pro Met Phe Ile Gly Gly Val Leu Phe Phe Ala Ile Phe Gln	305	310	315
Thr Gln Phe Thr Val Leu Ala Val Tyr Ser Asp Thr Arg Leu Asp Arg	325	330	335

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Asn Phe Phe Gly Ile Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn
340 345 350

Pro Ile Phe Ile Ile Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr
355 360 365

Lys Leu Gly Ala Lys Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala
370 375 380

Asn Ile Val Ile Gly Cys Ala Leu Phe Phe Phe Leu Pro Phe Ala Gly
385 390 395 400

Gly Ala Glu Asn Ser Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe
405 410 415

Leu Phe Thr Ile Ala Glu Leu Leu Leu Ser Pro Val Gly Asn Ser Leu
420 425 430

Ala Thr Lys Val Ala Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val
435 440 445

Trp Leu Met Ala Val Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly
450 455 460

Gly Tyr Tyr Asp Pro Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile
465 470 475 480

Thr Val Gly Val Ala Ala Ile Val Leu Gly Ala Ile Val Ile Ala Ala
485 490 495

Lys Gly Trp Val Leu Lys Lys Phe Ile Asp Val Arg
500 505

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<211> 1426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (93)..(1403)
<223> RXA02394

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ttctgcaagt tcagcgaag gtaggaacta atatg ttg tcg cca gca gct gta 113
Met Leu Ser Pro Ala Ala Val
1 5

gca gct tta att ctt gtc atc ggc att gtg gtg ctc atc atc gca tca 161
Ala Ala Leu Ile Leu Val Ile Gly Ile Val Val Leu Ile Ile Ala Ser
10 15 20

gtg ccc gtt gcc att gcc atc ggt ttg cca tca ctt ttt gcc gcg atg 209
Val Pro Val Ala Ile Ala Ile Gly Leu Pro Ser Leu Phe Ala Ala Met
25 30 35

gcc gtg ctt ggc cca gaa aac gcc gcg cag gcc gtc gcg cag cgc atg 257

280 285 290 295

ctg tcg tgg gtg atg gcc ttt gcc aag atc cct cag atg atc tct gat 1025
 Leu Ser Trp Val Met Ala Phe Ala Lys Ile Pro Gln Met Ile Ser Asp
 300 305 310

gcg ctt ctt tcg gta tcc gat tcc aag gtt gtc atc ttg ttg atc atg 1073
 Ala Leu Leu Ser Val Ser Asp Ser Lys Val Val Ile Leu Leu Ile Met
 315 320 325

atg ttc atc ctg tta ctc atc ggt acc gta atg gac cca aca cca gca 1121
 Met Phe Ile Leu Leu Leu Ile Gly Thr Val Met Asp Pro Thr Pro Ala
 330 335 340

att ttg atc ttc gtc ccg atc ttc ctt cca gtg gtt acc gaa ctt ggt 1169
 Ile Leu Ile Phe Val Pro Ile Phe Leu Pro Val Val Thr Glu Leu Gly
 345 350 355

gtg gac cca gtc cac ttc ggt gcg atg gtg gta atg aac ctg tcc gtg 1217
 Val Asp Pro Val His Phe Gly Ala Met Val Val Met Asn Leu Ser Val
 360 365 370 375

ggc gtg att acc cca cca gta ggc aac gtg ttg ttc gtt ggt tcg caa 1265
 Gly Val Ile Thr Pro Pro Val Gly Asn Val Leu Phe Val Gly Ser Gln
 380 385 390

gtg gca ggg ctg cgt gtg gaa act gtg atc aga cga ctg tgg ccg tat 1313
 Val Ala Gly Leu Arg Val Glu Thr Val Ile Arg Arg Leu Trp Pro Tyr
 395 400 405

ctc att gcc att att gtt gcg ctg ttc gtg gtt gtt ttc gta ccg cag 1361
 Leu Ile Ala Ile Ile Val Ala Leu Phe Val Val Val Phe Val Pro Gln
 410 415 420

atc tct atc tgg ctg ccc aca aca atg gga ttg atg gga ggc 1403
 Ile Ser Ile Trp Leu Pro Thr Thr Met Gly Leu Met Gly Gly
 425 430 435

taaacctcca gccatcagct aag 1426

<210> 180
 <211> 437
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 180
 Met Leu Ser Pro Ala Ala Val Ala Ala Leu Ile Leu Val Ile Gly Ile
 1 5 10 15
 Val Val Leu Ile Ile Ala Ser Val Pro Val Ala Ile Ala Ile Gly Leu
 20 25 30
 Pro Ser Leu Phe Ala Ala Met Ala Val Leu Gly Pro Glu Asn Ala Ala
 35 40 45
 Gln Ala Val Ala Gln Arg Met Phe Thr Gly Thr Asn Ser Phe Thr Leu
 50 55 60
 Leu Ala Ile Pro Phe Phe Val Leu Ala Gly Leu Leu Met Asn Ser Gly
 65 70 75 80

Gly	Ile	Ala	Thr	Arg 85	Leu	Ile	Asp	Ala	Ala	Lys	Val	Leu	Val	Gly	Arg
Met	Pro	Ala	Ser 100	Met	Ala	Asn	Thr	Asn 105	Ile	Ala	Ala	Asn	Gly 110	Leu	Phe
Gly	Ala	Val 115	Ser	Gly	Ala	Ala	Val 120	Ala	Ser	Ala	Ser	Ala 125	Val	Gly	Thr
Val	Met 130	Thr	Pro	Lys	Met	Lys 135	Glu	Glu	Gly	Tyr	Ser 140	Arg	Ala	Tyr	Ala
Ala 145	Ala	Val	Asn	Val	Ala 150	Ser	Ala	Pro	Ala	Gly 155	Met	Leu	Ile	Pro	Pro 160
Ser	Asn	Thr	Phe 165	Ile	Val	Tyr	Ser	Leu 170	Val	Ser	Ser	Thr	Ser	Ile 175	Ala
Ala	Leu	Phe 180	Met	Ala	Gly	Val	Gly 185	Pro	Gly	Leu	Leu	Trp	Ile 190	Leu	Ala
Cys	Val 195	Ile	Val	Gly	Thr	Trp	Leu 200	Ala	Arg	Lys	Glu	Asn 205	Tyr	Lys	Arg
Glu 210	Gln	Ile	His	Pro	Thr	Phe 215	Lys	Gln	Ser	Leu	Val 220	Val	Leu	Trp	Arg
Ala 225	Leu	Pro	Ser	Leu	Leu 230	Met	Ile	Val	Ile	Val 235	Val	Gly	Gly	Ile	Leu 240
Leu	Gly	Trp	Phe 245	Thr	Pro	Thr	Glu	Ser	Ala 250	Ala	Ile	Ala	Val	Val 255	Tyr
Cys	Leu	Val 260	Leu	Gly	Phe	Ile	Tyr 265	Arg	Thr	Ile	Lys	Val	Gly 270	Asp	Leu
Ala	Asp 275	Ile	Leu	Leu	Lys	Ala	Thr 280	Arg	Thr	Thr	Ser	Ile 285	Val	Met	Leu
Leu 290	Ile	Ala	Val	Ser	Ala 295	Ala	Leu	Ser	Trp	Val	Met 300	Ala	Phe	Ala	Lys
Ile 305	Pro	Gln	Met	Ile	Ser 310	Asp	Ala	Leu	Leu	Ser 315	Val	Ser	Asp	Ser	Lys 320
Val	Val	Ile	Leu	Leu 325	Ile	Met	Met	Phe	Ile 330	Leu	Leu	Leu	Ile	Gly 335	Thr
Val	Met	Asp 340	Pro	Thr	Pro	Ala	Ile 345	Leu	Ile	Phe	Val	Pro	Ile 350	Phe	Leu
Pro	Val 355	Val	Thr	Glu	Leu	Gly	Val 360	Asp	Pro	Val	His	Phe 365	Gly	Ala	Met
Val 370	Val	Met	Asn	Leu	Ser	Val 375	Gly	Val	Ile	Thr	Pro 380	Pro	Val	Gly	Asn
Val 385	Leu	Phe	Val	Gly	Ser 390	Gln	Val	Ala	Gly	Leu 395	Arg	Val	Glu	Thr	Val 400

Ile Arg Arg Leu Trp Pro Tyr Leu Ile Ala Ile Ile Val Ala Leu Phe
 405 410 415

Val Val Val Phe Val Pro Gln Ile Ser Ile Trp Leu Pro Thr Thr Met
 420 425 430

Gly Leu Met Gly Gly
 435

<210> 181

<211> 1764

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1741)

<223> RXA01012

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caactaccta agccgcatca ttcagaagga ggcataaaaa atg act act ccc ttg 115
 Met Thr Thr Pro Leu
 1 5

tta gag atc aac gat ctg gtt gtc tcc tat caa act gct aaa ggt ttg 163
 Leu Glu Ile Asn Asp Leu Val Val Ser Tyr Gln Thr Ala Lys Gly Leu
 10 15 20

gtg cat gct gtc aac aat gtc agc ctg gag gtg cac cct ggc caa atc 211
 Val His Ala Val Asn Asn Val Ser Leu Glu Val His Pro Gly Gln Ile
 25 30 35

acc gcg att gtt ggt gag tcc ggt tct ggt aag tcc acc acc gct cag 259
 Thr Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Gln
 40 45 50

gcc gtg att ggt ttg ctg gct gat aat gct gaa gtg gat tct ggt cgg 307
 Ala Val Ile Gly Leu Leu Ala Asp Asn Ala Glu Val Asp Ser Gly Arg
 55 60 65

att tct ttc aac ggc cgt tcc ctt gtt ggc ttg aac gca cgt gag tgg 355
 Ile Ser Phe Asn Gly Arg Ser Leu Val Gly Leu Asn Ala Arg Glu Trp
 70 75 80 85

aaa aac gtt cgc ggt acc aaa att ggt ttg att ccg cag gac ccc aac 403
 Lys Asn Val Arg Gly Thr Lys Ile Gly Leu Ile Pro Gln Asp Pro Asn
 90 95 100

aac tct ctg aac ccg gtg aaa act atc ggc gct tca gtg ggg gag ggc 451
 Asn Ser Leu Asn Pro Val Lys Thr Ile Gly Ala Ser Val Gly Glu Gly
 105 110 115

ttg gct atc cac aag cgt gga acc gcc gcc gag cgc aaa aag aag gtc 499
 Leu Ala Ile His Lys Arg Gly Thr Ala Ala Glu Arg Lys Lys Lys Val
 120 125 130

att gag ctt cta gag cgc gtg ggt att gat aac cca gag gtc cgc tat 547
 Ile Glu Leu Leu Glu Arg Val Gly Ile Asp Asn Pro Glu Val Arg Tyr

135	140	145	
gac cag tac ccg cat gag ctg tct ggt ggc atg aag cag cgc gcg ttg			595
Asp Gln Tyr Pro His Glu Leu Ser Gly Gly Met Lys Gln Arg Ala Leu			
150	155	160	165
att gcc gct gcc att gca ctt gaa cca gag ctg atc att gcc gat gag			643
Ile Ala Ala Ala Ile Ala Leu Glu Pro Glu Leu Ile Ile Ala Asp Glu			
	170	175	180
ccc aca tct gcg ctg gat gtg acc gtg cag aaa att att ctc gat ctg			691
Pro Thr Ser Ala Leu Asp Val Thr Val Gln Lys Ile Ile Leu Asp Leu			
	185	190	195
ctg gaa gac atg cag cgt gaa ttg ggc atg ggt att ttg ttc att act			739
Leu Glu Asp Met Gln Arg Glu Leu Gly Met Gly Ile Leu Phe Ile Thr			
	200	205	210
cac gat cta gcc gtg gca ggc gat cgg gcg gat cgc atc gtc gtc atg			787
His Asp Leu Ala Val Ala Gly Asp Arg Ala Asp Arg Ile Val Val Met			
	215	220	225
caa aaa ggc gag gtg cgc gaa agt ggt tac gcg gct tcg gtc ttg acc			835
Gln Lys Gly Glu Val Arg Glu Ser Gly Tyr Ala Ala Ser Val Leu Thr			
	230	235	240
gac ccc cag cat gag tat tcc aag aag ttg ctt gcc gac gcg ccc tcc			883
Asp Pro Gln His Glu Tyr Ser Lys Lys Leu Leu Ala Asp Ala Pro Ser			
	250	255	260
ctc acc atc ggc gag atc ccc acg cga gtt ccg gcc gta gat ccg gag			931
Leu Thr Ile Gly Glu Ile Pro Thr Arg Val Pro Ala Val Asp Pro Glu			
	265	270	275
gta gcg cag gcc aaa ggc ccg ctt ctg gta gtg gat aaa ttc cgc aag			979
Val Ala Gln Ala Lys Gly Pro Leu Leu Val Val Asp Lys Phe Arg Lys			
	280	285	290
gaa cac caa cga ggc aaa gaa gga gca ttt gtt gcc gca aat gat att			1027
Glu His Gln Arg Gly Lys Glu Gly Ala Phe Val Ala Ala Asn Asp Ile			
	295	300	305
tcc ttc gaa gta ctg cct ggc acc acg cat gcc atc gtc ggt gaa tcc			1075
Ser Phe Glu Val Leu Pro Gly Thr Thr His Ala Ile Val Gly Glu Ser			
	310	315	320
ggt tct ggt aaa acc acg ctt ggc cgc gcg atc gcg atg ttt aat acg			1123
Gly Ser Gly Lys Thr Thr Leu Gly Arg Ala Ile Ala Met Phe Asn Thr			
	330	335	340
ccg acc tct ggt tcc att tca gta agt ggc aag gac atc acc aac ctg			1171
Pro Thr Ser Gly Ser Ile Ser Val Ser Gly Lys Asp Ile Thr Asn Leu			
	345	350	355
tcc aag gcc cag cag ccg gaa ctg cgc cag caa atc cag ctg gtg tac			1219
Ser Lys Ala Gln Gln Arg Glu Leu Arg Gln Gln Ile Gln Leu Val Tyr			
	360	365	370
caa aac ccg tat tct tcc ctg gat cct cgc caa acc att ggc tcc acc			1267
Gln Asn Pro Tyr Ser Ser Leu Asp Pro Arg Gln Thr Ile Gly Ser Thr			
	375	380	385

atc gcg gaa cct ctg cgc aat ttc acc aag gtg agc aag cag gaa gcc 1315
 Ile Ala Glu Pro Leu Arg Asn Phe Thr Lys Val Ser Lys Gln Glu Ala
 390 395 400 405
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 Asp Glu Lys Val Ala His Tyr Leu Glu Leu Val Ala Leu Asp Pro Ala
 410 415 420
 ctt gcc acc cgt cgc cca cgt gag ctc tct ggt ggt cag cgc cag cgc 1411
 Leu Ala Thr Arg Arg Pro Arg Glu Leu Ser Gly Gly Gln Arg Gln Arg
 425 430 435
 gtc gcc att gct cgt gcc atg att ttg gaa cct gaa ttg gtg gtt ttc 1459
 Val Ala Ile Ala Arg Ala Met Ile Leu Glu Pro Glu Leu Val Val Phe
 440 445 450
 gac gaa gcc gta tcc gcg ttg gat gtg act gtg cag gca caa atc ctg 1507
 Asp Glu Ala Val Ser Ala Leu Asp Val Thr Val Gln Ala Gln Ile Leu
 455 460 465
 cgc ctg ctc gac gat ctg caa cga gag cta ggc ttg act tac gtg ttt 1555
 Arg Leu Leu Asp Asp Leu Gln Arg Glu Leu Gly Leu Thr Tyr Val Phe
 470 475 480 485
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 Ile Ser His Asp Leu Ala Val Val Arg Glu Ile Ser Asp Thr Val Ser
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 gtg atg agt cgc ggc aac cag gtg gaa ctt gga aaa acc gca gaa gta 1651
 Val Met Ser Arg Gly Asn Gln Val Glu Leu Gly Lys Thr Ala Glu Val
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 Phe Asn Asn Pro Gln Thr Asp Phe Thr Arg Arg Leu Ile Asp Ala Ile
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<213> Corynebacterium glutamicum

<400> 182

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 Ser Thr Thr Ala Gln Ala Val Ile Gly Leu Leu Ala Asp Asn Ala Glu
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Val 65	Asp	Ser	Gly	Arg	Ile 70	Ser	Phe	Asn	Gly	Arg 75	Ser	Leu	Val	Gly	Leu 80
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Pro	Gln	Asp	Pro 100	Asn	Asn	Ser	Leu	Asn 105	Pro	Val	Lys	Thr	Ile 110	Gly	Ala
Ser	Val	Gly 115	Glu	Gly	Leu	Ala	Ile 120	His	Lys	Arg	Gly	Thr 125	Ala	Ala	Glu
Arg	Lys 130	Lys	Lys	Val	Ile	Glu 135	Leu	Leu	Glu	Arg	Val 140	Gly	Ile	Asp	Asn
Pro 145	Glu	Val	Arg	Tyr	Asp 150	Gln	Tyr	Pro	His 155	Glu	Leu	Ser	Gly	Gly	Met 160
Lys	Gln	Arg	Ala	Leu 165	Ile	Ala	Ala	Ala	Ile 170	Ala	Leu	Glu	Pro	Glu 175	Leu
Ile	Ile	Ala	Asp 180	Glu	Pro	Thr	Ser	Ala 185	Leu	Asp	Val	Thr	Val 190	Gln	Lys
Ile	Ile 195	Leu	Asp	Leu	Leu	Glu	Asp 200	Met	Gln	Arg	Glu 205	Leu	Gly	Met	Gly
Ile 210	Leu	Phe	Ile	Thr	His	Asp 215	Leu	Ala	Val	Ala	Gly 220	Asp	Arg	Ala	Asp
Arg 225	Ile	Val	Val	Met	Gln 230	Lys	Gly	Glu	Val	Arg 235	Glu	Ser	Gly	Tyr	Ala 240
Ala	Ser	Val	Leu	Thr 245	Asp	Pro	Gln	His	Glu 250	Tyr	Ser	Lys	Lys	Leu 255	Leu
Ala	Asp	Ala	Pro 260	Ser	Leu	Thr	Ile	Gly 265	Glu	Ile	Pro	Thr	Arg 270	Val	Pro
Ala	Val 275	Asp	Pro	Glu	Val	Ala	Gln 280	Ala	Lys	Gly	Pro	Leu 285	Leu	Val	Val
Asp 290	Lys	Phe	Arg	Lys	Glu	His 295	Gln	Arg	Gly	Lys	Glu 300	Gly	Ala	Phe	Val
Ala 305	Ala	Asn	Asp	Ile	Ser 310	Phe	Glu	Val	Leu	Pro 315	Gly	Thr	Thr	His	Ala 320
Ile	Val	Gly	Glu	Ser 325	Gly	Ser	Gly	Lys	Thr 330	Thr	Leu	Gly	Arg	Ala 335	Ile
Ala	Met	Phe 340	Asn	Thr	Pro	Thr	Ser	Gly 345	Ser	Ile	Ser	Val	Ser 350	Gly	Lys
Asp	Ile	Thr 355	Asn	Leu	Ser	Lys	Ala 360	Gln	Gln	Arg	Glu	Leu 365	Arg	Gln	Gln
Ile	Gln 370	Leu	Val	Tyr	Gln 375	Asn	Pro	Tyr	Ser	Ser 380	Leu	Asp	Pro	Arg	Gln

Thr Ile Gly Ser Thr Ile Ala Glu Pro Leu Arg Asn Phe Thr Lys Val
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 Ser Lys Gln Glu Ala Asp Glu Lys Val Ala His Tyr Leu Glu Leu Val
 405 410 415
 Ala Leu Asp Pro Ala Leu Ala Thr Arg Arg Pro Arg Glu Leu Ser Gly
 420 425 430
 Gly Gln Arg Gln Arg Val Ala Ile Ala Arg Ala Met Ile Leu Glu Pro
 435 440 445
 Glu Leu Val Val Phe Asp Glu Ala Val Ser Ala Leu Asp Val Thr Val
 450 455 460
 Gln Ala Gln Ile Leu Arg Leu Leu Asp Asp Leu Gln Arg Glu Leu Gly
 465 470 475 480
 Leu Thr Tyr Val Phe Ile Ser His Asp Leu Ala Val Val Arg Glu Ile
 485 490 495
 Ser Asp Thr Val Ser Val Met Ser Arg Gly Asn Gln Val Glu Leu Gly
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 Lys Thr Ala Glu Val Phe Asn Asn Pro Gln Thr Asp Phe Thr Arg Arg
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 Met Ile Ile Gly Val
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 acc ctg ctg gtt ttc atc gtc atg tca ttc tct cct gcc gac ccg gca 163
 Thr Leu Leu Val Phe Ile Val Met Ser Phe Ser Pro Ala Asp Pro Ala
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 cga ctt gcc cta ggc gaa tca gcc tcc ccc gaa gca ctt gaa gcc tac 211
 Arg Leu Ala Leu Gly Glu Ser Ala Ser Pro Glu Ala Leu Glu Ala Tyr
 25 30 35
 cgt gaa gcc aac ggc ctc aac gat cca atg atg gtt cgc tat ttc gac 259
 Arg Glu Ala Asn Gly Leu Asn Asp Pro Met Met Val Arg Tyr Phe Asp

40 45 50
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 Phe Ile Leu Gly Met Leu Lys Gly Asp Leu Gly Thr Ser Ser Gly Gly
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 gta gct gtt acc gac att gtt gcc cgc gct ttc ccc atc acc ctg cag 355
 Val Ala Val Thr Asp Ile Val Ala Arg Ala Phe Pro Ile Thr Leu Gln
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 cta aca ttc tgg gga ctc atc atc gct gtt gta gtg gcg ttg atc ctc 403
 Leu Thr Phe Trp Gly Leu Ile Ile Ala Val Val Val Ala Leu Ile Leu
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 Gly Val Ile Ala Ala Leu Tyr Arg Asp Arg Trp Pro Asp Gln Leu Ile
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 Arg Val Val Ser Ile Ala Ala Leu Ala Thr Pro Ser Phe Trp Leu Ala
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 atc ttg ctg atc cag tgg ttg ggt act atc cct gga gcc tgg ggt ttc 547
 Ile Leu Leu Ile Gln Trp Leu Gly Thr Ile Pro Gly Ala Trp Gly Phe
 135 140 145
 ttc cca gca ctt gtc acc cgg tgg gtc cca ttc agc gaa gat ccc gcc 595
 Phe Pro Ala Leu Val Thr Arg Trp Val Pro Phe Ser Glu Asp Pro Ala
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 acc tac ttc aac aac atc gca ctt cag cga ttg cgt tgg cag tcc ccg 643
 Thr Tyr Phe Asn Asn Ile Ala Leu Gln Arg Leu Arg Trp Gln Ser Pro
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 ttg cag gtt ctt tgg ccc gcg ttg ttc gta cct cca tgg tgg aag aac 691
 Leu Gln Val Leu Trp Pro Ala Leu Phe Val Pro Pro Trp Trp Lys Asn
 185 190 195
 tgg aca agg act acg tcc gca cag caa tcg gtg cag gat ccc caa aac 739
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<213> Corynebacterium glutamicum

<400> 184

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 Val Arg Tyr Phe Asp Phe Ile Leu Gly Met Leu Lys Gly Asp Leu Gly

50 55 60

Thr Ser Ser Gly Gly Val Ala Val Thr Asp Ile Val Ala Arg Ala Phe
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Pro Ile Thr Leu Gln Leu Thr Phe Trp Gly Leu Ile Ile Ala Val Val
85 90 95

Val Ala Leu Ile Leu Gly Val Ile Ala Ala Leu Tyr Arg Asp Arg Trp
100 105 110

Pro Asp Gln Leu Ile Arg Val Val Ser Ile Ala Ala Leu Ala Thr Pro
115 120 125

Ser Phe Trp Leu Ala Ile Leu Leu Ile Gln Trp Leu Gly Thr Ile Pro
130 135 140

Gly Ala Trp Gly Phe Phe Pro Ala Leu Val Thr Arg Trp Val Pro Phe
145 150 155 160

Ser Glu Asp Pro Ala Thr Tyr Phe Asn Asn Ile Ala Leu Gln Arg Leu
165 170 175

Arg Trp Gln Ser Pro Leu Gln Val Leu Trp Pro Ala Leu Phe Val Pro
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Gln Asp Pro Gln Asn
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Val Ile Gly Leu Arg
1 5

gtt ggt tcc ctc atg ggt ggt gcg gtg atc att gag atc atc ttc aac 163
Val Gly Ser Leu Met Gly Gly Ala Val Ile Ile Glu Ile Ile Phe Asn
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atc caa gca atg gga cag ctc atc cta gac ggt gtg acc cga aat gac 211
Ile Gln Ala Met Gly Gln Leu Ile Leu Asp Gly Val Thr Arg Asn Asp
25 30 35

gtc tac ctc gtc caa ggt gtc acc ctc acc gtt gcc atc gcc ttc atc 259
Val Tyr Leu Val Gln Gly Val Thr Leu Thr Val Ala Ile Ala Phe Ile
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Ile Arg Ser Ile
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<400> 186
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Ala Trp Thr Val Leu Arg Tyr Thr Leu Thr Phe Val Ile Ala Ser Ile
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atc att ttt gtg ctg att cga gtc atc ccc ggt gac ccc gcc gct gtt 211
Ile Ile Phe Val Leu Ile Arg Val Ile Pro Gly Asp Pro Ala Ala Val
25 30 35

gcc ctg gga att acc gcg aca cca gaa gca atc gct gcg ttg caa tca 259
Ala Leu Gly Ile Thr Ala Thr Pro Glu Ala Ile Ala Ala Leu Gln Ser
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 310 315 320

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Asp Pro Ala Ala Val Ala Leu Gly Ile Thr Ala Thr Pro Glu Ala Ile
 35 40 45

Ala Ala Leu Gln Ser Gln Leu Gly Thr Asp Gln Pro Leu Phe Gln Gln
 50 55 60

Tyr Phe Ser Trp Ile Gly Gly Met Leu Thr Gly Asp Phe Gly Thr Ser
 65 70 75 80

Leu Ser Ser Gly Gln Asp Leu Ser Pro Ile Ile Phe Asp Arg Leu Gln
 85 90 95

Val Ser Leu Ile Leu Val Gly Cys Ser Ile Val Leu Ser Leu Leu Ile
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Ala Ile Pro Leu Gly Val Leu Ser Ala Arg Arg Gly Gly Val Ile Ile
 115 120 125

Ser Gly Ile Ser Gln Ile Gly Ile Ala Ile Pro Ser Phe Leu Ala Gly
 130 135 140

Ile Leu Leu Val Ala Val Phe Ala Val Gly Leu Gly Trp Leu Pro Ala
 145 150 155 160

Asn Gly Trp Ile Pro Pro Ser Glu Asn Phe Gly Gly Phe Leu Ala Arg
 165 170 175

Leu Ile Leu Pro Val Leu Ala Leu Thr Ala Val Gln Ala Ala Ile Leu
 180 185 190

Thr Arg Tyr Val Arg Ser Ala Val Met Asp Val Met Gly Gln Asp Phe
 195 200 205

Met Arg Thr Ala Arg Ser Lys Gly Met Ser Phe Asn Arg Ala Leu Ile
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Ile His Gly Leu Arg Asn Ala Ala Leu Pro Val Leu Thr Val Thr Gly
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Val Ala

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Leu	Ala	Val	Ala	Val	Leu	Met	Ala	Leu	Val	Pro	Gly	Leu	Phe	Thr	Ser	
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cag gat ccg ttc act ggc gat gat gtg gcg ctg ctt ggg cca agt ggc																144
Gln	Asp	Pro	Phe	Thr	Gly	Asp	Asp	Val	Ala	Leu	Leu	Gly	Pro	Ser	Gly	
		35					40					45				
acc cac tgg ttt ggt acc gat tcc gtg gga cgc gat ctc tac agt cgt																192
Thr	His	Trp	Phe	Gly	Thr	Asp	Ser	Val	Gly	Arg	Asp	Leu	Tyr	Ser	Arg	
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gtt gtt tac ggc gcg agg gaa acc ctg ctc ggt gca ctg atc gca gtg																240
Val	Val	Tyr	Gly	Ala	Arg	Glu	Thr	Leu	Leu	Gly	Ala	Leu	Ile	Ala	Val	
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ctg gtt ggt ctg atc gtg gga acc ctg atc gga ctg ctc gca ggt gca																288
Leu	Val	Gly	Leu	Ile	Val	Gly	Thr	Leu	Ile	Gly	Leu	Leu	Ala	Gly	Ala	
				85				90					95			
cag cgc ggt tgg gtt gac act gta tta atg cgt ttc gtg gat gtg ctg																336
Gln	Arg	Gly	Trp	Val	Asp	Thr	Val	Leu	Met	Arg	Phe	Val	Asp	Val	Leu	
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ttg tcc atc ccg gca ctg ctg ctc agc ttg act gtc att atc ctt ttg																384
Leu	Ser	Ile	Pro	Ala	Leu	Leu	Leu	Ser	Leu	Thr	Val	Ile	Ile	Leu	Leu	
		115					120					125				

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 Gly Phe Gly Thr Met Asn Ala Ala Ile Ala Val Gly Ile Thr Ser Val
 130 135 140

gcc acc ttc gcg cgt ctg gcg cgt tcc cag gtg atg act gtt gca ggt 480
 Ala Thr Phe Ala Arg Leu Ala Arg Ser Gln Val Met Thr Val Ala Gly
 145 150 155 160

tcc gat ttc gtg gaa gct gca tac ggt tcc ggt ggc acc cag gcg cag 528
 Ser Asp Phe Val Glu Ala Ala Tyr Gly Ser Gly Gly Thr Gln Ala Gln
 165 170 175

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 Val Leu Phe Arg His Ile Leu Pro Asn Ser Leu Thr Pro Val Phe Ala
 180 185 190

ctt gca gca ctg cag ttc ggt tcc gcg att ttg cag ctg tcc gtg ttg 624
 Leu Ala Ala Leu Gln Phe Gly Ser Ala Ile Leu Gln Leu Ser Val Leu
 195 200 205

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 Gly Phe Leu Gly Tyr Gly Ala Pro Ala Pro Thr Pro Glu Trp Gly Leu
 210 215 220

ctg atc tct gat gcc cgc gac tac atg gcg acc tca tgg tgg ctg act 720
 Leu Ile Ser Asp Ala Arg Asp Tyr Met Ala Thr Ser Trp Trp Leu Thr
 225 230 235 240

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 Val Leu Pro Gly Phe Val Ile Ile Ala Val Val Met Ser Ala Asn Tyr
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gtt 818

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<211> 265

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

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Gln Asp Pro Phe Thr Gly Asp Asp Val Ala Leu Leu Gly Pro Ser Gly
 35 40 45

Thr His Trp Phe Gly Thr Asp Ser Val Gly Arg Asp Leu Tyr Ser Arg
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Val Val Tyr Gly Ala Arg Glu Thr Leu Leu Gly Ala Leu Ile Ala Val
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                                         Met Pro Leu Ser Gly
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aaa atc ggc ggc ttc atc gtt gcc gtt gta ttt gtt ctt gct gcg ctg 163
Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe Val Leu Ala Ala Leu
                        10                        15                        20

tct ttc att tgg act ccg ttt gat cca gtt caa gct ttc cca cag gag 211
Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln Ala Phe Pro Gln Glu
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Leu	Gly	Ile	Ala	Ala	Gly	Met	Arg	Arg	Gly	Met	Val	Glu	Thr	Phe	Val	
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Met	Arg	Gly	Ala	Asp	Leu	Met	Leu	Ala	Phe	Pro	Ala	Leu	Leu	Leu	Ala	
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Ala	Ile	Gly	Ile	Ala	Gly	Ile	Pro	Ser	Phe	Ala	Arg	Val	Ala	Arg	Ala	
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ggc	aca	ttg	cag	gtg	acc	agt	cag	gat	ttc	atc	gca	gct	gct	cgg	cta	595
Gly	Thr	Leu	Gln	Val	Thr	Ser	Gln	Asp	Phe	Ile	Ala	Ala	Ala	Arg	Leu	
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Ser	Lys	Val	Ser	Ser	Ala	Arg	Ile	Ala	Leu	Arg	His	Ile	Leu	Pro	Asn	
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Ile	Thr	Ser	Met	Leu	Ile	Val	Gln	Ala	Ser	Val	Ala	Phe	Ala	Leu	Ala	
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Pro	Asp	Pro	Ser	Trp	Gly	Arg	Met	Leu	Gln	Thr	Ala	Gln	Ala	Ser	Ile	
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ggc	gtc	acc	ccc	atg	ttg	gcg	gtg	tgg	ccc	ggt	gct	gcg	atc	gct	ttg	835
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933

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Gly	Thr	Asp	Arg	Tyr	Gly	Arg	Asp	Val	Leu	Ser	Gln	Ile	Met	Val	Gly	
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Val	Glu	Thr	Phe	Val	Met	Arg	Gly	Ala	Asp	Leu	Met	Leu	Ala	Phe	Pro	
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Trp	Ser	Ala	Met	Val	Ala	Ile	Gly	Ile	Ala	Gly	Ile	Pro	Ser	Phe	Ala	
	130					135					140					
Arg	Val	Ala	Arg	Ala	Gly	Thr	Leu	Gln	Val	Thr	Ser	Gln	Asp	Phe	Ile	
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Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile Ala Ala Ala Arg Leu
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Ala Phe Pro Gln Glu Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu
35 40 45

Gly Thr Asp Arg Tyr Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly
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Ser Arg Val Thr Leu Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala
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Val Glu Thr Phe Val Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro
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Ala Leu Leu Leu Ala Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr
115 120 125

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Trp Leu Gly Ile Ile Leu Ile Gln Ile Val Ser Phe Arg Leu Gly Trp				
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Asn Ala Leu Leu Pro Thr Leu Thr Ile Ala Gly Ile Leu Phe Gly Glu				
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9095100

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Pro	Ala	Phe	Ala	Leu	Ile	Ala	Glu	Arg	Arg	Met	Glu	Ser	Val	Phe	Val	
				90					95					100		
atg	ctg	att	gtt	gcg	gtt	tgc	caa	ggc	ttt	gcg	acg	gtt	gcg	ttc	cag	451
Met	Leu	Ile	Val	Ala	Val	Cys	Gln	Gly	Phe	Ala	Thr	Val	Ala	Phe	Gln	
			105					110					115			
acc	gtc	acc	aac	aac	cgc	att	atc	acg	ccg	tcg	atc	atg	ggc	ttt	gaa	499
Thr	Val	Thr	Asn	Asn	Arg	Ile	Ile	Thr	Pro	Ser	Ile	Met	Gly	Phe	Glu	
		120				125						130				
tct	ctc	tac	aca	ctg	att	cat	acc	tcc	aca	gtg	ttc	ttc	ttc	ggc	gca	547
Ser	Leu	Tyr	Thr	Leu	Ile	His	Thr	Ser	Thr	Val	Phe	Phe	Phe	Gly	Ala	
	135					140					145					
act	gca	ctg	ctg	gcc	acc	aga	aat	ctc	gaa	atg	ttt	gtc	ggc	cag	ctg	595
Thr	Ala	Leu	Leu	Ala	Thr	Arg	Asn	Leu	Glu	Met	Phe	Val	Gly	Gln	Leu	
	150				155					160					165	
gtg	atc	atg	gtt	ctt	ttg	acc	ttg	gtc	ctc	tac	acc	tgg	ctg	ctt	tcc	643
Val	Ile	Met	Val	Leu	Leu	Thr	Leu	Val	Leu	Tyr	Thr	Trp	Leu	Leu	Ser	
				170					175					180		
gga	aaa	cgc	ggc	gat	atg	cac	gcc	atg	ctg	ctt	gtc	ggc	atc	atc	att	691
Gly	Lys	Arg	Gly	Asp	Met	His	Ala	Met	Leu	Leu	Val	Gly	Ile	Ile	Ile	
			185					190					195			
ggt	ggc	gga	ctc	gga	tcc	atc	tcc	acc	ttt	atg	cag	cgc	att	ctg	acc	739
Gly	Gly	Gly	Leu	Gly	Ser	Ile	Ser	Thr	Phe	Met	Gln	Arg	Ile	Leu	Thr	
		200					205					210				
cca	tca	gaa	ttc	gat	att	ctt	tcc	gcc	cga	ctt	ttc	gga	tca	gta	aac	787
Pro	Ser	Glu	Phe	Asp	Ile	Leu	Ser	Ala	Arg	Leu	Phe	Gly	Ser	Val	Asn	
	215					220					225					
aac	gcg	gaa	acc	gaa	tac	ttc	cca	att	gct	gtt	cca	cta	gta	gta	gtg	835
Asn	Ala	Glu	Thr	Glu	Tyr	Phe	Pro	Ile	Ala	Val	Pro	Leu	Val	Val	Val	
	230				235					240					245	
gcg	tcc	gtc	ttg	ttg	ctg	cta	agc	tct	cga	cgc	ctc	aac	gtt	gta	ggg	883
Ala	Ser	Val	Leu	Leu	Leu	Leu	Ser	Ser	Arg	Arg	Leu	Asn	Val	Val	Gly	
				250					255					260		
ctt	ggc	aaa	gat	gcc	gca	acc	aac	ctt</								

tgattacgtt aactaatgtc cgc 1242

Phe Val Gly Gln Leu Val Ile Met Val Leu Leu Thr Leu Val Leu Tyr
165 170 175

Thr Trp Leu Leu Ser Gly Lys Arg Gly Asp Met His Ala Met Leu Leu
 180 185 190
 Val Gly Ile Ile Ile Gly Gly Gly Leu Gly Ser Ile Ser Thr Phe Met
 195 200 205
 Gln Arg Ile Leu Thr Pro Ser Glu Phe Asp Ile Leu Ser Ala Arg Leu
 210 215 220
 Phe Gly Ser Val Asn Asn Ala Glu Thr Glu Tyr Phe Pro Ile Ala Val
 225 230 235 240
 Pro Leu Val Val Val Ala Ser Val Leu Leu Leu Leu Ser Ser Arg Arg
 245 250 255
 Leu Asn Val Val Gly Leu Gly Lys Asp Ala Ala Thr Asn Leu Gly Ile
 260 265 270
 Asn His Arg Arg Ser Ser Ile Tyr Thr Leu Val Leu Val Ser Val Leu
 275 280 285
 Met Ala Val Ser Thr Ala Leu Val Gly Pro Met Thr Phe Leu Gly Phe
 290 295 300
 Leu Val Ala Thr Leu Ala Tyr Gln Phe Ala Asp Thr Tyr Asp His Arg
 305 310 315 320
 Tyr Ile Leu Pro Met Ser Ala Leu Ile Gly Phe Val Val Leu Ser Gly
 325 330 335
 Ala Tyr Phe Val Met Asn His Val Phe Arg Ala Gln Gly Val Val Ser
 340 345 350
 Ile Ile Ile Glu Met Val Gly Gly Thr Val Phe Leu Ile Val Ile Leu
 355 360 365
 Arg Lys Gly Arg Leu
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1099)
 <223> RXA00089

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 Met Ala Thr Pro Ala
 1 5
 tcg gct ccc act tcc gaa cca cgt ctc aaa cgc acc aga gcc aag ctt 163
 Ser Ala Pro Thr Ser Glu Pro Arg Leu Lys Arg Thr Arg Ala Lys Leu
 10 15 20

ttt gat tgg aag ctt ctc atc ggc atc att ttc gtc gcc ggc ctc gtg	211
Phe Asp Trp Lys Leu Leu Ile Gly Ile Ile Phe Val Ala Gly Leu Val	
25 30 35	
gtg ctt tcc ctc ctc acc ggc caa tac gac att ttc ggt ggc gat gat	259
Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile Phe Gly Gly Asp Asp	
40 45 50	
ggc caa ctg atg ttc gag gca gtt cgc atc ccg cgt acc gtt tcc ctc	307
Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro Arg Thr Val Ser Leu	
55 60 65	
att ttg tcc ggt gca gca atg gcg atg tgt ggc tta gtc atg cag ctg	355
Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly Leu Val Met Gln Leu	
70 75 80 85	
ttg acc caa aac aaa ttc gtg gaa ccc agc acc aca gga aca acc gaa	403
Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr Thr Gly Thr Thr Glu	
90 95 100	
tgg gca ggt ctt ggc ctc ctc ttc gtg att tac ttc gtg cca gcc gcg	451
Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr Phe Val Pro Ala Ala	
105 110 115	
acc gtt ttg gat cgc atg ctc ggt gcc gtg gtg ttt tcc ttc atc gga	499
Thr Val Leu Asp Arg Met Leu Gly Ala Val Val Phe Ser Phe Ile Gly	
120 125 130	
acc atg gtg ttc ttc ctc ttt cta cgc cga gta aca ctg cgt tcc tca	547
Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val Thr Leu Arg Ser Ser	
135 140 145	
ttg atc gtc ccg att atc ggc atc atg ctc ggt gcc gtg gtg tca tcc	595
Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly Ala Val Val Ser Ser	
150 155 160 165	
atc tcc agc ttc ttc gcc ttg caa ttc gac atg ctc cag caa ttg gga	643
Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met Leu Gln Gln Leu Gly	
170 175 180	
aca tgg ttt gcg ggt tcc ttt aat aca gtg ttc cgc gga cag tac gaa	691
Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe Arg Gly Gln Tyr Glu	
185 190 195	
gtg ctg tgg atc gtt gtc atc gtc gtt att gca gtg ttc ttc ttc gca	739
Val Leu Trp Ile Val Val Ile Val Val Ile Ala Val Phe Phe Phe Ala	
200 205 210	
gac cgg ctc acc gta gct ggc ctt ggc gag gaa atc gcg aca aac gtg	787
Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu Ile Ala Thr Asn Val	
215 220 225	
ggt ctc aat tac aac cgc atg gtc ctt atc gga act ggc ctc atc gcc	835
Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly Thr Gly Leu Ile Ala	
230 235 240 245	
atc gca aca ggt gtg gtc acc gtc gtg gtt ggt agc ctg cca ttc ctc	883
Ile Ala Thr Gly Val Val Thr Val Val Val Gly Ser Leu Pro Phe Leu	
250 255 260	

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<211> 333
<212> PRT
<213> *Corynebacterium glutamicum*

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Thr Arg Ala Lys Leu Phe Asp Trp Lys Leu Leu Ile Gly Ile Ile Phe
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Val Ala Gly Leu Val Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile
35 40 45
Phe Gly Gly Asp Asp Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro
50 55 60
Arg Thr Val Ser Leu Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly
65 70 75 80
Leu Val Met Gln Leu Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr
85 90 95
Thr Gly Thr Thr Glu Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr
100 105 110
Phe Val Pro Ala Ala Thr Val Leu Asp Arg Met Leu Gly Ala Val Val
115 120 125
Phe Ser Phe Ile Gly Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val
130 135 140
Thr Leu Arg Ser Ser Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly
145 150 155 160
Ala Val Val Ser Ser Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met
165 170 175
Leu Gln Gln Leu Gly Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe

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180 185 190

Arg Gly Gln Tyr Glu Val Leu Trp Ile Val Val Ile Val Val Ile Ala
195 200 205

Val Phe Phe Phe Ala Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu
210 215 220

Ile Ala Thr Asn Val Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly
225 230 235 240

Thr Gly Leu Ile Ala Ile Ala Thr Gly Val Val Thr Val Val Val Gly
245 250 255

Ser Leu Pro Phe Leu Gly Leu Ile Val Pro Asn Val Val Ser Met Phe
260 265 270

Arg Gly Asp Asp Leu Arg Ser Asn Leu Pro Trp Val Cys Leu Thr Gly
275 280 285

Ile Ala Ile Val Thr Ile Cys Asp Leu Ile Ser Arg Thr Ile Ile Ala
290 295 300

Pro Phe Glu Ile Pro Val Ser Val Ile Leu Gly Ile Ile Gly Ala Val
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Val Phe Val Ile Met Ile Val Arg Gln Arg Gly Arg Gly
325 330

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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(726)
<223> RXN01285

<400> 203

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aac ggc tgc ggc aaa tcc acc ctg ctc cgc ggt ttc tcc cgc gtg ctc	96
Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu	
20 25 30	
aat ccg cag cac ggc aaa gtg ctt ctc gac ggt cgg caa ctc gat tca	144
Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser	
35 40 45	
ttc aag cct aaa gag atc gcc cga gaa cta ggc ctg ctg cca cag acc	192
Phe Lys Pro Lys Glu Ile Ala Arg Glu Leu Gly Leu Leu Pro Gln Thr	
50 55 60	
tcc atc gcc cca gaa ggc atc cgg gtt tac gat ctc atc gcg cgc ggg	240
Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile Ala Arg Gly	
65 70 75 80	

cgc gct ccc tac caa agc ctc ata caa caa tgg cgc acc tcc gac gaa 288
 Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr Ser Asp Glu
 85 90 95

gac gcc gtc gcg caa gcg ctc gcc tcc acg aat ctc acc gaa ctt gca 336
 Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr Glu Leu Ala
 100 105 110

gct cgc ctc gtc gat gaa ctc tcc ggt ggc cag cgc caa cga gtg tgg 384
 Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Trp
 115 120 125

gtg gcc atg ttg ctc gcc cag caa aca ccg atc atg ctt ctc gac gag 432
 Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu Leu Asp Glu
 130 135 140

ccc acc acc ttc ctc gac atc gcc cac caa tac gaa ctc ttg gaa ttg 480
 Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu Leu Glu Leu
 145 150 155 160

ctg cgc gca ttc aac gag gcc ggg aaa act gtg gtc act gtg ctt cac 528
 Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr Val Leu His
 165 170 175

gat ctc aac caa gcc gcc cgc tac gcc gac cac ctc atc gtg atg aaa 576
 Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile Val Met Lys
 180 185 190

gat ggg cac gta cat gcc acg ggc aca ccg gag gaa gtc tta act gcc 624
 Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val Leu Thr Ala
 195 200 205

gag atg gtt caa gga gtt ttt ggc ctg ccc tgc atc atc tcc cca gac 672
 Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile Ser Pro Asp
 210 215 220

ccc gtc aca gga acc ccc acc gtc gtt ccc ctc agt cgg tct cgc gca 720
 Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg Ser Arg Ala
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 Gly Ala

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<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

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Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu
 20 25 30

Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser
 35 40 45

Phe Lys Pro Lys Glu Ile Ala Arg Glu Leu Gly Leu Leu Pro Gln Thr

50 55 60

Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile Ala Arg Gly
65 70 75 80

Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr Ser Asp Glu
85 90 95

Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr Glu Leu Ala
100 105 110

Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Trp
115 120 125

Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu Leu Asp Glu
130 135 140

Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu Leu Glu Leu
145 150 155 160

Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr Val Leu His
165 170 175

Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile Val Met Lys
180 185 190

Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val Leu Thr Ala
195 200 205

Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile Ser Pro Asp
210 215 220

Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg Ser Arg Ala
225 230 235 240

Gly Ala

<210> 205
<211> 566
<212> DNA
<213> Corynebacterium glutamicum

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<222> (1)..(543)
<223> FRXA01285

<400> 205

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1				5					10					15		

gcg	cgc	ggg	cgc	gct	ccc	tac	caa	agc	ctc	ata	caa	caa	tgg	cgc	acc	96
Ala	Arg	Gly	Arg	Ala	Pro	Tyr	Gln	Ser	Leu	Ile	Gln	Gln	Trp	Arg	Thr	
			20					25					30			

tcc	gac	gaa	gac	gcc	gtc	gcg	caa	gcg	ctc	gcc	tcc	acg	aat	ctc	acc	144
Ser	Asp	Glu	Asp	Ala	Val	Ala	Gln	Ala	Leu	Ala	Ser	Thr	Asn	Leu	Thr	
		35					40					45				

gaa ctt gca gct cgc ctc gtc gat gaa ctc tcc ggt ggc cag cgc caa 192
 Glu Leu Ala Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln
 50 55 60
 cga gtg tgg gtg gcc atg ttg ctc gcc cag caa aca ccg atc atg ctt 240
 Arg Val Trp Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu
 65 70 75 80
 ctc gac gag ccc acc acc ttc ctc gac atc gcc cac caa tac gaa ctc 288
 Leu Asp Glu Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu
 85 90 95
 ttg gaa ttg ctg cgc gca ttc aac gag gcc ggg aaa act gtg gtc act 336
 Leu Glu Leu Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr
 100 105 110
 gtg ctt cac gat ctc aac caa gcc gcc cgc tac gcc gac cac ctc atc 384
 Val Leu His Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile
 115 120 125
 gtg atg aaa gat ggg cac gta cat gcc acg ggc aca ccg gag gaa gtc 432
 Val Met Lys Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val
 130 135 140
 tta act gcc gag atg gtt caa gga gtt ttt ggc ctg ccc tgc atc atc 480
 Leu Thr Ala Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile
 145 150 155 160
 tcc cca gac ccc gtc aca gga acc ccc acc gtc gtt ccc ctc agt cgg 528
 Ser Pro Asp Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg
 165 170 175
 tct cgc gca gga gct taagtagcta cccctccaac gga 566
 Ser Arg Ala Gly Ala
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<210> 206

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

Pro Gln Thr Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile
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 20 25 30
 Ser Asp Glu Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr
 35 40 45
 Glu Leu Ala Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln
 50 55 60
 Arg Val Trp Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu
 65 70 75 80
 Leu Asp Glu Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu
 85 90 95

Leu	Glu	Leu	Leu	Arg	Ala	Phe	Asn	Glu	Ala	Gly	Lys	Thr	Val	Val	Thr	
			100				105						110			
Val	Leu	His	Asp	Leu	Asn	Gln	Ala	Ala	Arg	Tyr	Ala	Asp	His	Leu	Ile	
			115				120						125			
Val	Met	Lys	Asp	Gly	His	Val	His	Ala	Thr	Gly	Thr	Pro	Glu	Glu	Val	
			130				135						140			
Leu	Thr	Ala	Glu	Met	Val	Gln	Gly	Val	Phe	Gly	Leu	Pro	Cys	Ile	Ile	
145						150						155			160	
Ser	Pro	Asp	Pro	Val	Thr	Gly	Thr	Pro	Thr	Val	Val	Pro	Leu	Ser	Arg	
			165						170						175	
Ser	Arg	Ala	Gly	Ala												
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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA02728
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										atg	gcc	att	gtt	tcc		115
										Met	Ala	Ile	Val	Ser		
										1				5		
ctc gac aac gtc acc gta tcc att gaa gga aaa aag ctt ctc gac gcc																163
Leu	Asp	Asn	Val	Thr	Val	Ser	Ile	Glu	Gly	Lys	Lys	Leu	Leu	Asp	Ala	
				10					15					20		
gtc tcc ctc aag gcc tac ccc ggg gaa gtg ttg gga ctc atc ggc cca																211
Val	Ser	Leu	Lys	Ala	Tyr	Pro	Gly	Glu	Val	Leu	Gly	Leu	Ile	Gly	Pro	
			25				30						35			
aac ggt gcc gga aaa tcc act ctg ctg agt gtc ctt tca ggc gat cgg																259
Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Leu	Ser	Val	Leu	Ser	Gly	Asp	Arg	
		40					45					50				
ctt ccc gat tca ggc gaa gtc aac gtc ggt ggc tta gat ccc gca aca																307
Leu	Pro	Asp	Ser	Gly	Glu	Val	Asn	Val	Gly	Gly	Leu	Asp	Pro	Ala	Thr	
	55					60					65					
gca gcg gca tcc gat atg gcc agg gtg cga gca gtc atg ctt caa gat																355
Ala	Ala	Ala	Ser	Asp	Met	Ala	Arg	Val	Arg	Ala	Val	Met	Leu	Gln	Asp	
70					75					80					85	
gtc agc gtg gca ttt tcc ttc ctc gtg tgg gac gtc gta gaa atg ggc																403
Val	Ser	Val	Ala	Phe	Ser	Phe	Leu	Val	Trp	Asp	Val	Val	Glu	Met	Gly	
				90					95					100		

agg cgg ccg tgg cag aag gcg tca acc ccc gaa gag gat cat gaa atc 451
 Arg Arg Pro Trp Gln Lys Ala Ser Thr Pro Glu Glu Asp His Glu Ile
 105 110 115

atc gaa gca gcg ctt gcc gcc acc tcg gta tcg cac ctt gcc gaa cgt 499
 Ile Glu Ala Ala Leu Ala Ala Thr Ser Val Ser His Leu Ala Glu Arg
 120 125 130

gaa atc acc aca ctg tca ggc ggc gag cgg gca cgc gtt gcc ttg tcc 547
 Glu Ile Thr Thr Leu Ser Gly Gly Glu Arg Ala Arg Val Ala Leu Ser
 135 140 145

cgt gtc ctt gct cag caa acc ccc att gtg ctg ttg gac gaa cca aca 595
 Arg Val Leu Ala Gln Gln Thr Pro Ile Val Leu Leu Asp Glu Pro Thr
 150 155 160 165

gcc gcg atg gat atc agc cac caa gaa caa act ctg ggc aca gcg cga 643
 Ala Ala Met Asp Ile Ser His Gln Glu Gln Thr Leu Gly Thr Ala Arg
 170 175 180

gca ctg gca gcc gcc ggg gca gca gtg att gtg gtc ctt cat gat ctc 691
 Ala Leu Ala Ala Ala Gly Ala Ala Val Ile Val Val Leu His Asp Leu
 185 190 195

aat gcg gcc gct gca tat tgc gac agc att gtg tgt ctc agt gat ggt 739
 Asn Ala Ala Ala Tyr Cys Asp Ser Ile Val Cys Leu Ser Asp Gly
 200 205 210

cga gtg att gcc tcc ggt tct gtt gat cag gtg tat tcc acg gaa acg 787
 Arg Val Ile Ala Ser Gly Ser Val Asp Gln Val Tyr Ser Thr Glu Thr
 215 220 225

ctg tcc cgt gtt tac ggt tgg cct atc agg gtc gat cat agt gga aaa 835
 Leu Ser Arg Val Tyr Gln Trp Pro Ile Arg Val Asp His Ser Gly Lys
 230 235 240 245

tat gtt cga gtg gag ccg gac cgt tct gag gcg aat tta ccc tcc gta 883
 Tyr Val Arg Val Glu Pro Asp Arg Ser Glu Ala Asn Leu Pro Ser Val
 250 255 260

cta cag gtg aaa aat acg gtt tca cca gct tagatacatg actaactaag 933
 Leu Gln Val Lys Asn Thr Val Ser Pro Ala
 265 270

gtt 936

<210> 208
 <211> 271
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 208
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Lys Leu Leu Asp Ala Val Ser Leu Lys Ala Tyr Pro Gly Glu Val Leu
 20 25 30

Gly Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Val
 35 40 45

Leu Ser Gly Asp Arg Leu Pro Asp Ser Gly Glu Val Asn Val Gly Gly
50 55 60

Leu Asp Pro Ala Thr Ala Ala Ser Asp Met Ala Arg Val Arg Ala
65 70 75 80

Val Met Leu Gln Asp Val Ser Val Ala Phe Ser Phe Leu Val Trp Asp
85 90 95

Val Val Glu Met Gly Arg Arg Pro Trp Gln Lys Ala Ser Thr Pro Glu
100 105 110

Glu Asp His Glu Ile Ile Glu Ala Leu Ala Ala Thr Ser Val Ser
115 120 125

His Leu Ala Glu Arg Glu Ile Thr Thr Leu Ser Gly Gly Glu Arg Ala
130 135 140

Arg Val Ala Leu Ser Arg Val Leu Ala Gln Gln Thr Pro Ile Val Leu
145 150 155 160

Leu Asp Glu Pro Thr Ala Ala Met Asp Ile Ser His Gln Glu Gln Thr
165 170 175

Leu Gly Thr Ala Arg Ala Leu Ala Ala Ala Gly Ala Ala Val Ile Val
180 185 190

Val Leu His Asp Leu Asn Ala Ala Ala Ala Tyr Cys Asp Ser Ile Val
195 200 205

Cys Leu Ser Asp Gly Arg Val Ile Ala Ser Gly Ser Val Asp Gln Val
210 215 220

Tyr Ser Thr Glu Thr Leu Ser Arg Val Tyr Gly Trp Pro Ile Arg Val
225 230 235 240

Asp His Ser Gly Lys Tyr Val Arg Val Glu Pro Asp Arg Ser Glu Ala
245 250 255

Asn Leu Pro Ser Val Leu Gln Val Lys Asn Thr Val Ser Pro Ala
260 265 270

<210> 209

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(880)

<223> RXN03080

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Met Pro Gln Leu Val
1 5

gaa att cgt gat ctc aac gtt gaa ttc ccc tct cgc cat gca gtg aaa Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys 10 15 20																163
aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly 25 30 35																211
cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu 40 45 50																259
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gag cag ccc gtc aac gaa tta tcg ggc ggc cag cag cag ctc atc cac Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln Gln Gln Leu Ile His 135 140 145																547
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gac ggc gaa gtt gtc tcc caa ggt gac atc cgc gag gtg ctc gaa cct Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg Glu Val Leu Glu Pro 215 220 225																787
gcc aca ctg tcc acc gtg tac gga ctg ccc att gcg gtg cgc gat gat Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile Ala Val Arg Asp Asp 230 235 240 245																835
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903

 $\langle 400 \rangle$ 210

Pro Asn Pro Phe

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Met Pro Gln Leu Val 5																
gaa att cgt gat ctc aac gtt gaa ttc ccc tct cgc cat gca gtg aaa 163																
Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys 10 15 20																
aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc 211																
Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly 25 30 35																
cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg 259																
Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu 40 45 50																
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Val Glu Ser Thr Gly Glu Val Met Val Gly Gly Ser Gly Val Ala Ser 55 60 65																
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Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp Val Val Ala Met Gly 90 95 100																
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Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu Thr Asp Ala Asp Arg 105 110 115																
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Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn Ala Leu Asp Ile Ala 120 125 130																
gag cag ccc gtc aac gaa tta tcg ggc ggc cag cag cag ctc atc cac 547																
Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln Gln Gln Leu Ile His 135 140 145																
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Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val Val Leu Leu Asp Glu 150 155 160 165																
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Pro Val Ser Ala Leu Asp Leu Arg His Gln Val Glu Val Leu Gln Leu
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Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val Ile Val Val Leu His
185 190 195

gat ctc aac cac gtt gcc cgt tgg tgc gac cat gca gtg ttg atg gcc 739
Asp Leu Asn His Val Ala Arg Trp Cys Asp His Ala Val Leu Met Ala
200 205 210

gac ggc gaa gtt gtc tcc caa ggt gac atc cgc gag gtg ctc gaa cct 787
Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg Glu Val Leu Glu Pro
215 220 225

gcc aca ctg tcc acc gtg tac gga ctg ccc att gcg gtg cgc gat gat 835
Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile Ala Val Arg Asp Asp
230 235 240 245

ccc gaa acc agc tca ctt cgc gtg atc ccg cat cca aat ccc ttt 880
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<213> Corynebacterium glutamicum

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35 40 45

Ala Ile Ala Gly Leu Val Glu Ser Thr Gly Glu Val Met Val Gly Gly
50 55 60

Ser Gly Val Ala Ser Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser
65 70 75 80

Leu Val Pro Gln Asn Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp
85 90 95

Val Val Ala Met Gly Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu
100 105 110

Thr Asp Ala Asp Arg Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn
115 120 125

Ala Leu Asp Ile Ala Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln
130 135 140

Gln Gln Leu Ile His Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val
145 150 155 160

Val Leu Leu Asp Glu Pro Val Ser Ala Leu Asp Leu Arg His Gln Val
165 170 175

Glu Val Leu Gln Leu Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val
180 185 190

Ile Val Val Leu His Asp Leu Asn His Val Ala Arg Trp Cys Asp His
195 200 205

Ala Val Leu Met Ala Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg
210 215 220

Glu Val Leu Glu Pro Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile
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Pro Asn Pro Phe
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Met Ser Leu Ser His
1 5

caa ctc aag cgc cag cgc gca tcg cgc aac tcc cgc agg tgg ctg att 163
Gln Leu Lys Arg Gln Arg Ala Ser Arg Asn Ser Arg Arg Trp Leu Ile
10 15 20

gtt gcg gca ttg ggc gtc gtc acg ctt ggt att ttt gct ttt tct ttg 211
Val Ala Ala Leu Gly Val Val Thr Leu Gly Ile Phe Ala Phe Ser Leu
25 30 35

atg tgg ggc gag gtg ttt tat ggc cct gct cag gtg ctg aaa gtg ttg 259
Met Trp Gly Glu Val Phe Tyr Gly Pro Ala Gln Val Leu Lys Val Leu
40 45 50

tct gga cag cag gtt ccc ggc gcg agt tat tcc gtt ggc gtg ttg cgt 307
Ser Gly Gln Gln Val Pro Gly Ala Ser Tyr Ser Val Gly Val Leu Arg
55 60 65

ttg ccg cgc gcg gtg atg ggt ttg act gcg ggt ttg gcg ttt ggc gcg 355
Leu Pro Arg Ala Val Met Gly Leu Thr Ala Gly Leu Ala Phe Gly Ala
70 75 80 85

gcg ggc gtg att ttt cag acg gtg ttg cgt aat cag ttg gcg tcg ccg 403

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Asp	Ile	Ile	Gly	Ile	Ser	Ser	Gly	Ala	Ser	Ala	Ala	Gly	Val	Ile	Cys	
			105					110					115			
att	gtg	ttt	ttc	ggg	atg	tcg	cag	tct	gca	gtg	tcg	gcg	att	tct	ttg	499
Ile	Val	Phe	Phe	Gly	Met	Ser	Gln	Ser	Ala	Val	Ser	Ala	Ile	Ser	Leu	
		120					125						130			
tgt	gcg	tcc	ttg	gct	gtg	gcg	ttg	ttg	att	tat	ctg	gtg	gcg	tat	cgc	547
Cys	Ala	Ser	Leu	Ala	Val	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ala	Tyr	Arg	
	135						140					145				
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Gly	Gly	Phe	Ser	Ala	Thr	Arg	Leu	Ile	Leu	Thr	Gly	Ile	Gly	Ile	Ala	
	150					155				160					165	
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Ala	Met	Leu	Asn	Ser	Leu	Val	Ser	Tyr	Ser	Leu	Ser	Lys	Ala	Asp	Ser	
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tgg	gat	ctg	ccg	acc	gcg	acg	cgc	tgg	ctt	acc	ggc	tcg	ctc	aat	ggt	691
Trp	Asp	Leu	Pro	Thr	Ala	Thr	Arg	Trp	Leu	Thr	Gly	Ser	Leu	Asn	Gly	
			185					190					195			
gcg	acg	tgg	gat	cgt	gcg	atg	ccg	ctg	att	gtc	acc	act	gtg	gta	ctc	739
Ala	Thr	Trp	Asp	Arg	Ala	Met	Pro	Leu	Ile	Val	Thr	Thr	Val	Val	Leu	
		200					205					210				
att	ccg	ctg	ctg	gtg	gct	aat	gcg	cgc	aat	gtg	gat	ctt	atg	cgt	ttg	787
Ile	Pro	Leu	Leu	Val	Ala	Asn	Ala	Arg	Asn	Val	Asp	Leu	Met	Arg	Leu	
	215					220					225					
ggc	aat	gat	tcc	gcg	gtg	ggt	ttg	ggc	gtt	gct	act	aat	cgc	acg	cgc	835
Gly	Asn	Asp	Ser	Ala	Val	Gly	Leu	Gly	Val	Ala	Thr	Asn	Arg	Thr	Arg	
	230				235				240					245		
gtc	att	gcg	att	att	gcc	gct	gtt	gcg	ctc	atc	gcc	gtt	gct	acc	gct	883
Val	Ile	Ala	Ile	Ile	Ala	Ala	Val	Ala	Leu	Ile	Ala	Val	Ala	Thr	Ala	
				250					255					260		
gca	tgc	ggc	ccg	atc	gca	ttc	gtg	gcg	ttt	gtg	tct	ggc	ccc	att	gcc	931
Ala	Cys	Gly	Pro	Ile	Ala	Phe	Val	Ala	Phe	Val	Ser	Gly	Pro	Ile	Ala	
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gcg	cgc	att	tta	ggc	tcc	ggc	gga	tcg	ctc	atc	atc	ccc	tcc	gca	ctc	979
Ala	Arg	Ile	Leu	Gly	Ser	Gly	Gly	Ser	Leu	Ile	Ile	Pro	Ser	Ala	Leu	
		280					285					290				
atc	ggc	ggg	ttg	atc	gtg	ctc	atc	gcc	gac	cta	att	ggc	caa	tac	ttc	1027
Ile	Gly	Gly	Leu	Ile	Val	Leu	Ile	Ala	Asp	Leu	Ile	Gly	Gln	Tyr	Phe	
	295					300					305					
ctc	ggc	acc	cgc	tac	ccc	gtc	gga	gtt	gtc	acc	ggc	gca	ttc	ggc	gcc	1075
Leu	Gly	Thr	Arg	Tyr	Pro	Val	Gly	Val	Val	Thr	Gly	Ala	Phe	Gly	Ala	
	310				315					320					325	
cca	ttc	ctt	atc	tat	tta	ctc	att	cgt	tcc	aac	cgc	gcg	gga	gta	acc	1123
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340

1149

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Pro	Asp	Ile	Ile	Gly	Ile	Ser	Ser	Gly	Ala	Ser	Ala	Ala	Gly	Val	Ile	
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Cys	Ile	Val	Phe	Phe	Gly	Met	Ser	Gln	Ser	Ala	Val	Ser	Ala	Ile	Ser	
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Leu	Cys	Ala	Ser	Leu	Ala	Val	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ala	Tyr	
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Arg	Gly	Gly	Phe	Ser	Ala	Thr	Arg	Leu	Ile	Leu	Thr	Gly	Ile	Gly	Ile	
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Ala	Ala	Met	Leu	Asn	Ser	Leu	Val	Ser	Tyr	Ser	Leu	Ser	Lys	Ala	Asp	
75				80				85								
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Ser	Trp	Asp	Leu	Pro	Thr	Ala	Thr	Arg	Trp	Leu	Thr	Gly	Ser	Leu	Asn	
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Gly	Ala	Thr	Trp	Asp	Arg	Ala	Met	Pro	Leu	Ile	Val	Thr	Thr	Val	Val	
105			110				115				120					

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 Leu Gly Asn Asp Ser Ala Val Gly Leu Gly Val Ala Thr Asn Arg Thr
 140 145 150
 cgc gtc att gcg att att gcc gct gtt gcg ctc atc gcc gtt gct acc 533
 Arg Val Ile Ala Ile Ile Ala Ala Val Ala Leu Ile Ala Val Ala Thr
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 Ala Ala Cys Gly Pro Ile Ala Phe Val Ala Phe Val Ser Gly Pro Ile
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 Ala Ala Arg Ile Leu Gly Ser Gly Gly Ser Leu Ile Ile Pro Ser Ala
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 ctc atc ggc ggg ttg atc gtg ctc atc gcc gac cta att ggc caa tac 677
 Leu Ile Gly Gly Leu Ile Val Leu Ile Ala Asp Leu Ile Gly Gln Tyr
 205 210 215
 ttc ctc ggc acc cgc tac ccc gtc gga gtt gtc acc ggc gca ttc ggc 725
 Phe Leu Gly Thr Arg Tyr Pro Val Gly Val Val Thr Gly Ala Phe Gly
 220 225 230
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 Thr Leu
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<213> Corynebacterium glutamicum

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 35 40 45
 Leu Leu Ile Tyr Leu Val Ala Tyr Arg Gly Gly Phe Ser Ala Thr Arg
 50 55 60
 Leu Ile Leu Thr Gly Ile Gly Ile Ala Ala Met Leu Asn Ser Leu Val
 65 70 75 80
 Ser Tyr Ser Leu Ser Lys Ala Asp Ser Trp Asp Leu Pro Thr Ala Thr
 85 90 95

Arg Trp Leu Thr Gly Ser Leu Asn Gly Ala Thr Trp Asp Arg Ala Met
 100 105 110

Pro Leu Ile Val Thr Thr Val Val Leu Ile Pro Leu Leu Val Ala Asn
 115 120 125

Ala Arg Asn Val Asp Leu Met Arg Leu Gly Asn Asp Ser Ala Val Gly
 130 135 140

Leu Gly Val Ala Thr Asn Arg Thr Arg Val Ile Ala Ile Ile Ala Ala
 145 150 155 160

Val Ala Leu Ile Ala Val Ala Thr Ala Ala Cys Gly Pro Ile Ala Phe
 165 170 175

Val Ala Phe Val Ser Gly Pro Ile Ala Ala Arg Ile Leu Gly Ser Gly
 180 185 190

Gly Ser Leu Ile Ile Pro Ser Ala Leu Ile Gly Gly Leu Ile Val Leu
 195 200 205

Ile Ala Asp Leu Ile Gly Gln Tyr Phe Leu Gly Thr Arg Tyr Pro Val
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Ile Arg Ser Asn Arg Ala Gly Val Thr Leu
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 Met Thr Ala Val Ala
 1 5

gta gag aag cag aag gag acg tcg ata agc aaa aac ctc ggc agg cgc 163
 Val Glu Lys Gln Lys Glu Thr Ser Ile Ser Lys Asn Leu Gly Arg Arg
 10 15 20

cga gcg ctg ggc att ctc gga atc gtc gtg gca ctg ggt gcg ctt att 211
 Arg Ala Leu Gly Ile Leu Gly Ile Val Val Ala Leu Gly Ala Leu Ile
 25 30 35

gtt tta agt att gct gtg ggt gcg aac cca ctt tct ttt agc tcc gta 259
 Val Leu Ser Ile Ala Val Gly Ala Asn Pro Leu Ser Phe Ser Ser Val
 40 45 50

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 Trp Gln Gly Phe Thr Ala His Asp Ser Ser Glu Ala Ser Ile Ile Val
 55 65

tgg tca atg cgt att ccg cgc acg ctg gtg ggc atc gtg act ggc gct 355
 Trp Ser Met Arg Ile Pro Arg Thr Leu Val Gly Ile Val Thr Gly Ala
 70 75 80

gct ttt ggt gtg gcg ggt gct tta att caa gcg ctg acg cgc aac ccg 403
 Ala Phe Gly Val Ala Gly Ala Leu Ile Gln Ala Leu Thr Arg Asn Pro
 90 95 100

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 Leu Ala Asp Pro Gly Ile Leu Gly Val Asn Ala Gly Ala Gly Phe Ala
 105 110 115

gtg acc gta ggt gtc gga ttt ttc gga ctc agc agc gtg acg ggc tac 499
 Val Thr Val Gly Val Gly Phe Gly Leu Ser Ser Val Thr Gly Tyr
 120 125 130

atc tgg ttc gca ttc ctg ggc gct gcc gcc gct acc ctg ctg gtg tat 547
 Ile Trp Phe Ala Phe Leu Gly Ala Ala Ala Thr Leu Leu Val Tyr
 135 140 145

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 Phe Ile Gly Ala Ser Thr Ser Gly Ser Val Asn Pro Val Ala Leu Val
 150 155 160 165

ctc gcc ggc gtt gct ctg gcc gcc gtg ctt ggt ggc gtc acg agc ttc 643
 Leu Ala Gly Val Ala Leu Ala Ala Val Leu Gly Gly Val Thr Ser Phe
 170 175 180

ctc aca ctg att gat cct gag act ttt gaa agc atc cgc aat tgg aat 691
 Leu Thr Leu Ile Asp Pro Glu Thr Phe Glu Ser Ile Arg Asn Trp Asn
 185 190 195

ctt ggt tct gtt gca cgc acc gac ctc agc gac acc atg acc gta ttg 739
 Leu Gly Ser Val Ala Arg Thr Asp Leu Ser Asp Thr Met Thr Val Leu
 200 205 210

cca ttc ctg gca gtc gga ctg gcc atc gcg ctc ctg ctg tcg gga gca 787
 Pro Phe Leu Ala Val Gly Leu Ala Ile Ala Leu Leu Leu Ser Gly Ala
 215 220 225

ctg aac tcc att gcg ctt ggc gat gac ctt gct gca tcc ctg ggc acc 835
 Leu Asn Ser Ile Ala Leu Gly Asp Asp Leu Ala Ala Ser Leu Gly Thr
 230 235 240 245

aaa gtg atg cgc acc cgc gtg ctc ggc atc att tca gtc acc ttg ttg 883
 Lys Val Met Arg Thr Arg Val Leu Gly Ile Ile Ser Val Thr Leu Leu
 250 255 260

gcc ggc ggc gcg acc gcc ctt act ggt ggt atc ggc ttc gta ggc ctt 931
 Ala Gly Gly Ala Thr Ala Leu Thr Gly Gly Ile Gly Phe Val Gly Leu
 265 270 275

atg gtt ccc cac gtt gtg cgc tgg gta gtt ggc ccc gat caa cga tgg 979
 Met Val Pro His Val Val Arg Trp Val Val Gly Pro Asp Asn Arg Trp
 280 285 290

atc atc acc ttc agc gcc ctg tgc gcc cct gtt ctt gta ctc ggc gca 1027

Ile Ile Thr Phe Ser Ala Leu Cys Ala Pro Val Leu Val Leu Gly Ala
 295 300 305

gac att ttg gga cgc atc atc gcc cgc ccc ggc gaa att gaa gta ggc 1075
 Asp Ile Leu Gly Arg Ile Ile Ala Arg Pro Gly Glu Ile Glu Val Gly
 310 315 320 325

att gtt acc gca gtc atc ggc gca cct gtc ctg atc gca cta gtt cga 1123
 Ile Val Thr Ala Val Ile Gly Ala Pro Val Leu Ile Ala Leu Val Arg
 330 335 340

cgg agg aaa gcc agt ggt ctt taatatcaaa tctagaactg atg 1167
 Arg Arg Lys Ala Ser Gly Leu
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<213> Corynebacterium glutamicum

<400> 218

Met Thr Ala Val Ala Val Glu Lys Gln Lys Glu Thr Ser Ile Ser Lys
 1 5 10 15

Asn Leu Gly Arg Arg Arg Ala Leu Gly Ile Leu Gly Ile Val Val Ala
 20 25 30

Leu Gly Ala Leu Ile Val Leu Ser Ile Ala Val Gly Ala Asn Pro Leu
 35 40 45

Ser Phe Ser Ser Val Trp Gln Gly Phe Thr Ala His Asp Ser Ser Glu
 50 55 60

Ala Ser Ile Ile Val Trp Ser Met Arg Ile Pro Arg Thr Leu Val Gly
 65 70 75 80

Ile Val Thr Gly Ala Ala Phe Gly Val Ala Gly Ala Leu Ile Gln Ala
 85 90 95

Leu Thr Arg Asn Pro Leu Ala Asp Pro Gly Ile Leu Gly Val Asn Ala
 100 105 110

Gly Ala Gly Phe Ala Val Thr Val Gly Val Gly Phe Phe Gly Leu Ser
 115 120 125

Ser Val Thr Gly Tyr Ile Trp Phe Ala Phe Leu Gly Ala Ala Ala Ala
 130 135 140

Thr Leu Leu Val Tyr Phe Ile Gly Ala Ser Thr Ser Gly Ser Val Asn
 145 150 155 160

Pro Val Ala Leu Val Leu Ala Gly Val Ala Leu Ala Ala Val Leu Gly
 165 170 175

Gly Val Thr Ser Phe Leu Thr Leu Ile Asp Pro Glu Thr Phe Glu Ser
 180 185 190

Ile Arg Asn Trp Asn Leu Gly Ser Val Ala Arg Thr Asp Leu Ser Asp
 195 200 205

Thr Met Thr Val Leu Pro Phe Leu Ala Val Gly Leu Ala Ile Ala Leu
 210 215 220
 Leu Leu Ser Gly Ala Leu Asn Ser Ile Ala Leu Gly Asp Asp Leu Ala
 225 230 235 240
 Ala Ser Leu Gly Thr Lys Val Met Arg Thr Arg Val Leu Gly Ile Ile
 245 250 255
 Ser Val Thr Leu Leu Ala Gly Gly Ala Thr Ala Leu Thr Gly Gly Ile
 260 265 270
 Gly Phe Val Gly Leu Met Val Pro His Val Val Arg Trp Val Val Gly
 275 280 285
 Pro Asp Gln Arg Trp Ile Ile Thr Phe Ser Ala Leu Cys Ala Pro Val
 290 295 300
 Leu Val Leu Gly Ala Asp Ile Leu Gly Arg Ile Ile Ala Arg Pro Gly
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 Glu Ile Glu Val Gly Ile Val Thr Ala Val Ile Gly Ala Pro Val Leu
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 340 345

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXA01290

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 gcacctgtcc tgatcgcaact agttcgacgg aggaaagcca gtg gtc ttt aat atc 115
 Val Val Phe Asn Ile
 1 5
 aaa tct aga act gat gaa act cct gtt gct gcg tct gag ccg gtg gaa 163
 Lys Ser Arg Thr Asp Glu Thr Pro Val Ala Ala Ser Glu Pro Val Glu
 10 15 20
 tcc act aga cct gtg tct gaa gct tcg aca agc cct gcg ctt aac ccc 211
 Ser Thr Arg Pro Val Ser Glu Ala Ser Thr Ser Pro Ala Leu Asn Pro
 25 30 35
 ggc tac cac gca gtt tca gtg cag agg cgc cgg ttc tct ttc cgc atc 259
 Gly Tyr His Ala Val Ser Val Gln Arg Arg Arg Phe Ser Phe Arg Ile
 40 45 50
 cca gcc cgc ctc atg gtg gtt agc ctt atc ctt ttc gcc atc gcg cta 307
 Pro Ala Arg Leu Met Val Val Ser Leu Ile Leu Phe Ala Ile Ala Leu
 55 60 65

tgc agc gcc aca tgg gct atc acg atg ggc gat tac cca ctg tct ttg	355
Cys Ser Ala Thr Trp Ala Ile Thr Met Gly Asp Tyr Pro Leu Ser Leu	
70 75 80 85	
ggg cag gtg att aat gca ctt gct ggc acc ggc gag aaa ttc cag ttg	403
Gly Gln Val Ile Asn Ala Leu Ala Gly Thr Gly Glu Lys Phe Gln Leu	
90 95 100	
ttg gtg gtg cgg gaa tgg cgt cta cct gta gcc att gct gct gtt gtc	451
Leu Val Val Arg Glu Trp Arg Leu Pro Val Ala Ile Ala Val Val	
105 110 115	
ttc ggc gcg ctg ctt ggc ata ggt gga gcg att ttc cag tcg att act	499
Phe Gly Ala Leu Leu Gly Ile Gly Gly Ala Ile Phe Gln Ser Ile Thr	
120 125 130	
cga aac ccg ttg ggt tca cct gac gtg att ggt ttc gat gca ggt tct	547
Arg Asn Pro Leu Gly Ser Pro Asp Val Ile Gly Phe Asp Ala Gly Ser	
135 140 145	
tac acg gcg gtg gtt ctt gtc att ttg gtc ctc ggc aac act cac tac	595
Tyr Thr Ala Val Val Leu Val Ile Leu Val Leu Gly Asn Thr His Tyr	
150 155 160 165	
tgg agc atc gct ttc gct gcc atc gtc ggt ggc att gtt acc gcc ttt	643
Trp Ser Ile Ala Phe Ala Ala Ile Val Gly Gly Ile Val Thr Ala Phe	
170 175 180	
gcc gtg tat gtc ctg gcg tgg cgt aaa ggt gtg caa ggt ttc cgc ttg	691
Ala Val Tyr Val Leu Ala Trp Arg Lys Gly Val Gln Gly Phe Arg Leu	
185 190 195	
atc atc gtg ggc atc ggt gtc tcg gcc atg ctc agt tcc gtt aac gcg	739
Ile Ile Val Gly Ile Gly Val Ser Ala Met Leu Ser Ser Val Asn Ala	
200 205 210	
tat cta atc acc cgc gcc gat gtg gaa gac gcc atg gtt gtg ggc ttc	787
Tyr Leu Ile Thr Arg Ala Asp Val Glu Asp Ala Met Val Val Gly Phe	
215 220 225	
tgg agt gcc ggt tcc atc aac cgc att acc tgg caa tct ctg ctc ccc	835
Trp Ser Ala Gly Ser Ile Asn Arg Ile Thr Trp Gln Ser Leu Leu Pro	
230 235 240 245	
tct ctg gtg atc gct gct gtc atc atc gtg gcc gcc att gtg ctg gca	883
Ser Leu Val Ile Ala Ala Val Ile Ile Val Ala Ala Ile Val Leu Ala	
250 255 260	
agg tca ctg cgt ttc atg gaa atg ggc gat gac gta gcc acc acc ctc	931
Arg Ser Leu Arg Phe Met Glu Met Gly Asp Asp Val Ala Thr Thr Leu	
265 270 275	
ggt gtg aaa aca aac tcc acc cgc ttg gca ctc atc gtt gtc ggc gtt	979
Gly Val Lys Thr Asn Ser Thr Arg Leu Ala Leu Ile Val Val Gly Val	
280 285 290	
gct acc tcc gcg ttg gtt aca gca gct gcc gga ccg atc tcc ttc atc	1027
Ala Thr Ser Ala Leu Val Thr Ala Ala Ala Gly Pro Ile Ser Phe Ile	
295 300 305	
gcg ttg gtt gcc cca cag ctg gca cgt cgc ctc act aaa acc cct ggt	1075

Ile Val Thr Ala Phe Ala Val Tyr Val Leu Ala Trp Arg Lys Gly Val
 180 185 190
 Gln Gly Phe Arg Leu Ile Ile Val Gly Ile Gly Val Ser Ala Met Leu
 195 200 205
 Ser Ser Val Asn Ala Tyr Leu Ile Thr Arg Ala Asp Val Glu Asp Ala
 210 215 220
 Met Val Val Gly Phe Trp Ser Ala Gly Ser Ile Asn Arg Ile Thr Trp
 225 230 235 240
 Gln Ser Leu Leu Pro Ser Leu Val Ile Ala Ala Val Ile Ile Val Ala
 245 250 255
 Ala Ile Val Leu Ala Arg Ser Leu Arg Phe Met Glu Met Gly Asp Asp
 260 265 270
 Val Ala Thr Thr Leu Gly Val Lys Thr Asn Ser Thr Arg Leu Ala Leu
 275 280 285
 Ile Val Val Gly Val Ala Thr Ser Ala Leu Val Thr Ala Ala Ala Gly
 290 295 300
 Pro Ile Ser Phe Ile Ala Leu Val Ala Pro Gln Leu Ala Arg Arg Leu
 305 310 315 320
 Thr Lys Thr Pro Gly Val Ser Leu Val Ala Ala Ala Ala Met Gly Ser
 325 330 335
 Ala Leu Leu Ser Cys Ala His Leu Leu Ser Leu Ile Ile Ser Ser Phe
 340 345 350
 Tyr Arg Thr Ile Pro Val Gly Leu Leu Thr Val Ser Ile Gly Gly Cys
 355 360 365
 Tyr Met Ile Trp Leu Leu Leu Arg Glu Thr Arg Arg Gln Tyr Arg Thr
 370 375 380
 Gly Thr Ile Arg
 385

<210> 221
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(582)
 <223> RXA01822

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 Met Ala Arg Gln Asn Ser Asn Thr Gly Gly Leu Arg Leu Val Leu Val
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 ggt atc gga aca ggt gca ttt ttg ggt gct gct cgt gat ttc ttc atg 96
 Gly Ile Gly Thr Gly Ala Phe Leu Gly Ala Ala Arg Asp Phe Phe Met
 20 25 30

[illegible]

<211> 194

<213> Corynebacterium glutamicum

Met Ala Arg Gln Asn Ser Asn Thr Gly Gly Leu Arg Leu Val Leu Val
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Gly Ile Gly Thr Gly Ala Phe Leu Gly Ala Ala Arg Asp Phe Phe Met
20 25 30

Val Arg Ala Asp Ile Thr Gly Ala Ser Thr Val Gln Leu Trp Ser Ala
35 40 45

Gly Ser Leu Ser Gly Arg Asp Trp Asn His Ala Leu Leu Val Leu Ile
 50 55 60
 Ser Cys Ala Val Ile Val Pro Ala Leu Cys Ile Ile Val Arg Arg Leu
 65 70 75 80
 Arg Leu Met Glu Met Gly Asp Asp Ala Ala Gly Ala Leu Gly Ile Ser
 85 90 95
 Val Glu Arg Thr Arg Leu Ile Ala Ile Leu Leu Ala Val Leu Leu Val
 100 105 110
 Gly Ile Ala Thr Ala Ala Ala Gly Pro Ile Ala Phe Ile Ala Leu Ala
 115 120 125
 Ala Pro Gln Ile Ala Arg Ala Leu Ala Arg Glu Asp Gly Val Leu Val
 130 135 140
 Ala Ala Ser Ile Ser Ile Gly Ser Gly Leu Leu Val Ala Ala Asp Cys
 145 150 155 160
 Leu Glu Gln His Val Asp Thr Glu Leu His Thr Pro Val Gly Leu Val
 165 170 175
 Thr Ser Leu Leu Gly Gly Val Tyr Leu Met Trp Leu Leu Ser Arg Lys
 180 185 190
 Glu Ala

<210> 223
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXN00466

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 gatagggttaa cctgattcga ttagaaaacg gagatttgtc gtg caa tcc cgc ctg 115
 Val Gln Ser Arg Leu
 1 5
 tcc aaa atc ctg cgc agt agc gtc gta ggc gtt gct gtc cta gcc ctg 163
 Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val Ala Val Leu Ala Leu
 10 15 20
 tta gct ggg tgt tct aac aat gca gat gac acc gac gct gat tca aca 211
 Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr Asp Ala Asp Ser Thr
 25 30 35
 tcc acg gga aac tcc gct ttt cct gtt tcg att gaa cac gag ttc gga 259
 Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile Glu His Glu Phe Gly
 40 45 50
 acc acc aca atc gat gat gta ccc gaa aga gtt gtc acc ctt ggc gtt 307

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<212> PRT
<213> Corynebacterium glutamicum
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Ala	Val	Leu	Ala	Leu	Leu	Ala	Gly	Cys	Ser	Asn	Asn	Ala	Asp	Asp	Thr
			20					25					30		
Asp	Ala	Asp	Ser	Thr	Ser	Thr	Gly	Asn	Ser	Ala	Phe	Pro	Val	Ser	Ile
		35					40					45			
Glu	His	Glu	Phe	Gly	Thr	Thr	Thr	Ile	Asp	Asp	Val	Pro	Glu	Arg	Val
	50					55					60				
Val	Thr	Leu	Gly	Val	Thr	Asp	Ala	Asp	Ile	Val	Leu	Ala	Leu	Gly	Thr
65					70					75					80
Val	Pro	Val	Gly	Asn	Thr	Gly	Tyr	Lys	Phe	Phe	Glu	Asn	Gly	Leu	Gly
				85					90					95	
Pro	Trp	Thr	Asp	Glu	Leu	Val	Glu	Gly	Lys	Glu	Leu	Thr	Leu	Leu	Asp
			100					105					110		
Ser	Asp	Ser	Thr	Pro	Asp	Leu	Glu	Gln	Val	Ala	Ala	Leu	Glu	Pro	Asp
		115					120					125			
Leu	Ile	Ile	Gly	Val	Ser	Ala	Gly	Phe	Asp	Asp	Val	Val	Tyr	Glu	Gln
	130					135					140				
Leu	Ser	Asp	Ile	Ala	Pro	Val	Val	Ala	Arg	Pro	Ala	Gly	Thr	Ala	Ala
145					150					155					160
Tyr	Ala	Val	Ala	Arg	Glu	Glu	Ala	Thr	Asn	Leu	Val	Ala	Arg	Ala	Met
				165					170					175	
Gly	Gln	Ser	Glu	Lys	Gly	Gln	Glu	Leu	Asn	Glu	Glu	Thr	Asp	Ala	Leu
			180					185					190		
Ile	Gln	Ala	Ala	Arg	Asp	Glu	Asn	Pro	Ser	Phe	Asp	Gly	Lys	Thr	Gly
		195					200					205			
Thr	Val	Ile	Leu	Pro	Tyr	Gln	Gly	Lys	Tyr	Gly	Ala	Tyr	Leu	Pro	Gly
	210					215					220				
Asp	Ala	Arg	Gly	Gln	Phe	Leu	Asp	Ser	Leu	Gly	Ile	Ser	Leu	Pro	Glu
225					230					235					240

290

295

300

Arg Gly Ala Ile Thr Tyr Asn Ser Val Leu Ser Val Pro Phe Ala Leu
 305 310 315 320

Glu His Leu Ala Pro Arg Ile Ala Glu
 325

<210> 227

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXN03081

<400> 227

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atccaaatcc cttttgattg aaagtttgac ttaaaaaccc atg aaa aaa tca ctc 115
 Met Lys Lys Ser Leu
 1 5

atc gcc att gtt gcc agt gcg ctc gtg tta agc ggc tgc acc tct gat 163
 Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser Gly Cys Thr Ser Asp
 10 15 20

tct tct gac tct tcc ggc act tcc gga act gtg gaa acc act tgc att 211
 Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val Glu Thr Thr Ser Ile
 25 30 35

aca acc agc gtt gcc gca gct gac ggc gca ttc cca cgc acc gtc aca 259
 Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe Pro Arg Thr Val Thr
 40 45 50

ctc gac gat tcc tcc atc acc tta gaa tcc aaa cca gag cgc atc gcc 307
 Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys Pro Glu Arg Ile Ala
 55 60 65

gta ctc acc cca gag gca gca tcc ttg gtt ctc ccc atc aca ggc gcc 355
 Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu Pro Ile Thr Gly Ala
 70 75 80 85

gac cgc gtc gtg atg acc gcc gaa atg gac acc gct gac gaa gaa acc 403
 Asp Arg Val Val Met Thr Ala Glu Met Asp Thr Ala Asp Glu Glu Thr
 90 95 100

gca gct ctg gcc tcc caa gtg gaa tac caa gtc aaa aac ggt ggc agg 451
 Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val Lys Asn Gly Gly Arg
 105 110 115

ctc gac ccc gaa caa gtt gtc gcc ggc gac cca gat ttg gtg atc gtc 499
 Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro Asp Leu Val Ile Val
 120 125 130

agt gcg cgt ttc gat acc gaa caa ggc acc atc gac att ttg gaa ggc 547
 Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile Asp Ile Leu Glu Gly
 135 140 145

582

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Met 1	Lys	Lys	Ser	Leu 5	Ile	Ala	Ile	Val	Ala 10	Ser	Ala	Leu	Val	Leu 15	Ser	
Gly	Cys	Thr	Ser 20	Asp	Ser	Ser	Asp	Ser 25	Ser	Gly	Thr	Ser	Gly 30	Thr	Val	
Glu	Thr	Thr 35	Ser	Ile	Thr	Thr	Ser 40	Val	Ala	Ala	Ala	Asp 45	Gly	Ala	Phe	
Pro 50	Arg	Thr	Val	Thr	Leu	Asp 55	Asp	Ser	Ser	Ile	Thr 60	Leu	Glu	Ser	Lys	
Pro 65	Glu	Arg	Ile	Ala	Val 70	Leu	Thr	Pro	Glu	Ala 75	Ala	Ser	Leu	Val	Leu 80	
Pro	Ile	Thr	Gly	Ala 85	Asp	Arg	Val	Val	Met 90	Thr	Ala	Glu	Met	Asp 95	Thr	
Ala	Asp	Glu	Glu 100	Thr	Ala	Ala	Leu	Ala 105	Ser	Gln	Val	Glu	Tyr 110	Gln	Val	
Lys	Asn	Gly 115	Gly	Arg	Leu	Asp	Pro 120	Glu	Gln	Val	Val	Ala 125	Gly	Asp	Pro	
Asp 130	Leu	Val	Ile	Val	Ser	Ala 135	Arg	Phe	Asp	Thr	Glu	Gln	Gly	Thr	Ile	
Asp 145	Ile	Leu	Glu	Gly 150	Leu	Asn	Val	Pro								

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<222> (101)..(1075)
<223> FRXA02863
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atccaaatcc cttttgattg aaagtttgac ttaaaaaccc atg aaa aaa tca ctc 115
                                         Met Lys Lys Ser Leu
                                         1                               5

atc gcc att gtt gcc aqt gcg ctc gtg tta agc qgc tgc acc tct gat 163

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[illegible]

250 255 260
 gag atc atc atc att cag gac ttc caa ggt aaa ggc cga gag aac ttc 931
 Glu Ile Ile Ile Ile Gln Asp Phe Gln Gly Lys Gly Arg Glu Asn Phe
 265 270 275
 gct aat ttc ctc tcc aac cca gcg cta gcc aac gtt ccc gcc att gaa 979
 Ala Asn Phe Leu Ser Asn Pro Ala Leu Ala Asn Val Pro Ala Ile Glu
 280 285 290
 aac gac aag att ttc tac gcc gac act gtc acc act gga gtt act gca 1027
 Asn Asp Lys Ile Phe Tyr Ala Asp Thr Val Thr Thr Gly Val Thr Ala
 295 300 305
 ggt acc gat atc acc act ggt ctg cag caa gtg gca gaa atg ctg agc 1075
 Gly Thr Asp Ile Thr Thr Gly Leu Gln Gln Val Ala Glu Met Leu Ser
 310 315 320 325
 tagttttgag atgttgaaac tag 1098

 <210> 230
 <211> 325
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 230
 Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser
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 Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val
 20 25 30
 Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe
 35 40 45
 Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys
 50 55 60
 Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu
 65 70 75 80
 Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr
 85 90 95
 Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val
 100 105 110
 Lys Asn Gly Gly Ser Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro
 115 120 125
 Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile
 130 135 140
 Asp Ile Leu Glu Gly Leu Asn Val Pro Val Val Asn Phe Asp Ser Asp
 145 150 155 160
 Ala Trp Gly Asp Ile Asp Ala Ile Thr Lys His Leu Glu Ile Val Gly
 165 170 175
 Glu Leu Val Gly Glu Glu Asp Lys Ala Ala Glu Ala Ile Ala Glu Ile

00000-400000

55 60 65

ggt gca ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc 355
 Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr
 70 75 80 85

gag ggt gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg 403
 Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala
 90 95 100

atg ttt ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc 451
 Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile
 105 110 115

atc tca ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt 499
 Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe
 120 125 130

gct cca tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc 547
 Ala Pro Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu
 135 140 145

gca gtt ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt 595
 Ala Val Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu
 150 155 160 165

gct cct ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg 643
 Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met
 170 175 180

att gtt gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga 691
 Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly
 185 190 195

aat gtt ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att 739
 Asn Val Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile
 200 205 210

gcc gca atc cca gca att gcc ctc ttc ttt gga atg 775
 Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly Met
 215 220 225

c 776

<210> 232

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Val Phe Arg Asp Pro Ala Pro Pro Ser Lys Gly Thr Thr Asn Leu Gly
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Asp Lys Met Ala Ser Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser
 20 25 30

Lys Lys Leu Pro Pro Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe
 35 40 45

Tyr Val Ala Leu Val Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp

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<223> FRXA01986
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gaa ggt ccg tat aga aag cgg cta ttc tac gtt gca cta gtt gcg acg 211
Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val Ala Leu Val Ala Thr
25 30 35

ttt ggt ggg ctg ctc ttc gga tat gac acc gga gta atc aac ggt gca 259
 Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly Val Ile Asn Gly Ala
 40 45 50

ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc gag ggt 307
 Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr Glu Gly
 55 60 65

gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg atg ttt 355
 Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala Met Phe
 70 75 80 85

ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc atc tca 403
 Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile Ile Ser
 90 95 100

ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt gct cca 451
 Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe Ala Pro
 105 110 115

tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc gca gtt 499
 Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu Ala Val
 120 125 130

ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt gct cct 547
 Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro
 135 140 145

ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg att gtt 595
 Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met Ile Val
 150 155 160 165

gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga aat gtt 643
 Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly Asn Val
 170 175 180

ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att gcc gca 691
 Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile Ala Ala
 185 190 195

atc cca gca att gcc ctc ttc ttt gga 718
 Ile Pro Ala Ile Ala Leu Phe Phe Gly
 200 205

<210> 234

<211> 206

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

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Ala Leu Val Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly
35 40 45

Val Ile Asn Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr

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<211> 1118
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXN02447
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1				5				10						15				
ggc	tcc	ctg	acc	ggc	cga	aac	gag	ctt	gct	atc	gtc	acc	ggc	cag	ctg	96		
Gly	Ser	Leu	Thr	Gly	Arg	Asn	Glu	Leu	Ala	Ile	Val	Thr	Gly	Gln	Leu			
			20						25						30			
ctt	gcc	ttc	gtg	atc	aac	gcg	ctt	atc	gcc	gtc	acc	cta	cac	gga	gtt	144		
Leu	Ala	Phe	Val	Ile	Asn	Ala	Leu	Ile	Ala	Val	Thr	Leu	His	Gly	Val			
		35						40						45				
att	gat	gga	atc	tgg	cgc	atc	atg	ttc	gcc	gtc	tgt	gcc	ctc	cct	gcc	192		
Ile	Asp	Gly	Ile	Trp	Arg	Ile	Met	Phe	Ala	Val	Cys	Ala	Leu	Pro	Ala			
50						55						60						
gtc	gcc	ctc	ttc	ctc	ggc	atg	ctg	cgg	atg	cgc	gaa	tca	cca	cgc	tgg	240		
Val	Ala	Leu	Phe	Leu	Gly	Met	Leu	Arg	Met	Pro	Glu	Ser	Pro	Arg	Trp			
65						70				75				80				

ctg	gtc	aac	cag	ggg	cgt	tac	gac	gac	gcc	cgc	cgc	gtc	atg	gag	acc	288
Leu	Val	Asn	Gln	Gly 85	Arg	Tyr	Asp	Asp	Ala 90	Arg	Arg	Val	Met	Glu 95	Thr	
gtc	cgt	acc	cct	gag	cgt	gcg	aaa	gcc	gaa	atg	gat	gaa	atc	atc	gcg	336
Val	Arg	Thr	Pro 100	Glu	Arg	Ala	Lys	Ala 105	Glu	Met	Asp	Glu	Ile 110	Ile	Ala	
gtg	cac	tct	gaa	aac	aat	gcg	gca	ctt	cct	ggt	gtt	aag	cag	tct	tcg	384
Val	His	Ser 115	Glu	Asn	Asn	Ala	Ala 120	Leu	Pro	Gly	Val	Lys 125	Gln	Ser	Ser	
ggc	cag	gct	tca	ggc	cag	gtt	tct	agc	aag	cac	acc	cac	atg	tcc	atc	432
Gly	Gln 130	Ala	Ser	Gly	Gln	Val 135	Ser	Ser	Lys	His	Thr 140	His	Met	Ser	Ile	
ggc	gaa	gtc	ctc	agc	aac	aaa	tgg	ctg	gtt	cgt	ctg	ctc	atc	gcc	ggc	480
Gly 145	Glu	Val	Leu	Ser	Asn 150	Lys	Trp	Leu	Val	Arg 155	Leu	Leu	Ile	Ala	Gly 160	
atc	ggt	gtt	gca	gtt	gcc	cag	cag	ctc	acc	ggc	atc	aac	gcc	atc	atg	528
Ile	Gly	Val	Ala 165	Val	Ala	Gln	Gln	Leu	Thr 170	Gly	Ile	Asn	Ala	Ile 175	Met	
tac	tac	gga	acc	cgc	gtc	ctc	gag	gaa	tcc	ggc	atg	agc	gca	gaa	atg	576
Tyr	Tyr	Gly 180	Thr	Arg	Val	Leu	Glu	Glu 185	Ser	Gly	Met	Ser	Ala 190	Glu	Met	
gct	gtg	gtt	gcc	aac	att	gct	ttc	ggt	gcc	gtt	gcc	gtc	atc	ggt	gga	624
Ala	Val	Val 195	Ala	Asn	Ile	Ala	Phe 200	Gly	Ala	Val	Ala	Val 205	Ile	Gly	Gly	
ctg	atc	gca	ctg	cgc	aac	atg	gac	cgc	ctg	gat	cgc	cgc	acc	acc	ttc	672
Leu	Ile 210	Ala	Leu	Arg	Asn	Met 215	Asp	Arg	Leu	Asp	Arg 220	Arg	Thr	Thr	Phe	
atc	atc	ggc	ctg	tca	ctg	acc	acc	acc	ttc	cac	ctt	ttg	atc	gca	gct	720
Ile 225	Ile	Gly	Leu	Ser	Leu 230	Thr	Thr	Thr	Phe	His 235	Leu	Leu	Ile	Ala	Ala 240	
gcc	ggc	act	ctc	ctt	cca	gaa	ggt	aac	tcc	att	cga	cca	ttc	gcc	atc	768
Ala	Gly	Thr	Leu 245	Leu	Pro	Glu	Gly	Asn	Ser 250	Ile	Arg	Pro	Phe	Ala 255	Ile	
atg	atc	ctt	gtt	gtt	ggg	ttc	gtg	ctc	tcc	atg	cag	act	ttc	ctc	aac	816
Met	Ile	Leu 260	Val	Val	Gly	Phe	Val 265	Leu	Ser	Met	Gln	Thr 270	Phe	Leu	Asn	
gtt	gca	gtg	tgg	gtg	tgg	ctg	gcg	gaa	atc	ttc	cca	gtc	cga	atg	aag	864
Val	Ala 275	Val	Trp	Val	Trp	Leu	Ala 280	Glu	Ile	Phe	Pro	Val 285	Arg	Met	Lys	
ggt	atc	ggc	acc	ggt	att	tcg	gta	ttc	tgc	ggt	tgg	ggc	atc	aat	ggc	912
Gly	Ile 290	Gly	Thr	Gly	Ile	Ser 295	Val	Phe	Cys	Gly	Trp 300	Gly	Ile	Asn	Gly	
gtc	cta	gcg	ttg	ttc	ttc	cca	gca	ctg	gtc	tcc	ggc	gtg	ggt	atc	acc	960
Val 305	Leu	Ala	Leu	Phe 310	Phe	Pro	Ala	Leu	Val	Ser 315	Gly	Val	Gly	Ile	Thr 320	
ttc	tcc	ttc	ctt	atc	ttc	gca	gtc	gtc	gga	gtc	att	gcc	ctg	gcg	ttc	1008

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<210> 236
<211> 365
<212> PRT
<213> Corynebacterium glutamicum
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Thr 1	Val	Val	Pro	Val 5	Tyr	Leu	Ala	Glu	Leu 10	Ala	Pro	Leu	Glu	Ile 15	Arg
Gly	Ser	Leu	Thr 20	Gly	Arg	Asn	Glu	Leu 25	Ala	Ile	Val	Thr	Gly 30	Gln	Leu
Leu	Ala	Phe 35	Val	Ile	Asn	Ala	Leu 40	Ile	Ala	Val	Thr	Leu 45	His	Gly	Val
Ile	Asp 50	Gly	Ile	Trp	Arg	Ile 55	Met	Phe	Ala	Val	Cys 60	Ala	Leu	Pro	Ala
Val 65	Ala	Leu	Phe	Leu	Gly 70	Met	Leu	Arg	Met	Pro 75	Glu	Ser	Pro	Arg	Trp 80
Leu	Val	Asn	Gln	Gly 85	Arg	Tyr	Asp	Asp	Ala 90	Arg	Arg	Val	Met	Glu 95	Thr
Val	Arg	Thr	Pro 100	Glu	Arg	Ala	Lys	Ala 105	Glu	Met	Asp	Glu	Ile 110	Ile	Ala
Val	His	Ser 115	Glu	Asn	Asn	Ala 120	Ala	Leu	Pro	Gly	Val	Lys 125	Gln	Ser	Ser
Gly	Gln 130	Ala	Ser	Gly	Gln	Val 135	Ser	Ser	Lys	His	Thr 140	His	Met	Ser	Ile
Gly 145	Glu	Val	Leu	Ser	Asn 150	Lys	Trp	Leu	Val	Arg 155	Leu	Leu	Ile	Ala	Gly 160
Ile	Gly	Val	Ala 165	Val	Ala	Gln	Gln	Leu 170	Thr	Gly	Ile	Asn	Ala 175	Ile	Met
Tyr	Tyr	Gly	Thr 180	Arg	Val	Leu	Glu	Glu 185	Ser	Gly	Met	Ser	Ala 190	Glu	Met
Ala	Val	Val 195	Ala	Asn	Ile	Ala	Phe 200	Gly	Ala	Val	Ala	Val 205	Ile	Gly	Gly
Leu	Ile 210	Ala	Leu	Arg	Asn 215	Met	Asp	Arg	Leu	Asp 220	Arg	Arg	Thr	Thr	Phe

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<210> 237
<211> 293
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(270)  
<223> FRXA02447
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<400> 237																	
tgg	gtg	tgg	ctg	gcg	gaa	atc	ttc	cca	gtc	cga	atg	aag	ggt	atc	ggc	48	
Trp	Val	Trp	Leu	Ala	Glu	Ile	Phe	Pro	Val	Arg	Met	Lys	Gly	Ile	Gly		
1				5					10					15			
acc	ggt	att	tcg	gta	ttc	tgc	ggt	tgg	ggc	atc	aat	ggc	gtc	cta	gcg	96	
Thr	Gly	Ile	Ser	Val	Phe	Cys	Gly	Trp	Gly	Ile	Asn	Gly	Val	Leu	Ala		
			20					25					30				
ttg	ttc	ttc	cca	gca	ctg	gtc	tcc	ggc	gtg	ggt	atc	acc	ttc	tcc	ttc	144	
Leu	Phe	Phe	Pro	Ala	Leu	Val	Ser	Gly	Val	Gly	Ile	Thr	Phe	Ser	Phe		
		35					40					45					
ctt	atc	ttc	gca	gtc	gtc	gga	gtc	att	gcc	ctg	gcg	ttc	gtc	acc	aag	192	
Leu	Ile	Phe	Ala	Val	Val	Gly	Val	Ile	Ala	Leu	Ala	Phe	Val	Thr	Lys		
	50					55					60						
ttt	gtt	cct	gaa	acc	cgt	ggc	cgc	tca	ctt	gaa	gaa	ctc	gat	cac	gca	240	
Phe	Val	Pro	Glu	Thr	Arg	Gly	Arg	Ser	Leu	Glu	Glu	Leu	Asp	His	Ala		
65					70					75					80		
gca	ttc	acc	ggc	cag	atc	ttc	aag	aag	gct	taa	acccccc	ctt	ccg	atctctt		290	

293

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<400> 238
Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys Gly Ile Gly
  1                               10                      15
Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly Val Leu Ala
      20                      25                      30
Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr Phe Ser Phe
      35                      40                      45
Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe Val Thr Lys
      50                      55                      60
Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu Asp His Ala
      65                      70                      75                      80
Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
      85                      90

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<220>  
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<222> (1)..(711)  
<223> FRXA02769
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<400> 239																
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Thr	Val	Val	Pro	Val	Tyr	Leu	Ala	Glu	Leu	Ala	Pro	Leu	Glu	Ile	Arg	
1				5					10					15		
ggc	tcc	ctg	acc	ggc	cga	aac	gag	ctt	gct	atc	gtc	acc	ggc	cag	ctg	96
Gly	Ser	Leu	Thr	Gly	Arg	Asn	Glu	Leu	Ala	Ile	Val	Thr	Gly	Gln	Leu	
			20					25					30			
ctt	gcc	ttc	gtg	atc	aac	gcg	ctt	atc	gcc	gtc	acc	cta	cac	gga	gtt	144
Leu	Ala	Phe	Val	Ile	Asn	Ala	Leu	Ile	Ala	Val	Thr	Leu	His	Gly	Val	
		35					40					45				
att	gat	gga	atc	tgg	cgc	atc	atg	ttc	gcc	gtc	tgt	gcc	ctc	cct	gcc	192
Ile	Asp	Gly	Ile	Trp	Arg	Ile	Met	Phe	Ala	Val	Cys	Ala	Leu	Pro	Ala	
	50					55					60					
gtc	gcc	ctc	ttc	ctc	ggc	atg	ctg	cgg	atg	ccg	gaa	tca	cca	cgc	tgg	240
Val	Ala	Leu	Phe	Leu	Gly	Met	Leu	Arg	Met	Pro	Glu	Ser	Pro	Arg	Trp	
65					70					75					80	

ctg gtc aac cag ggg cgt tac gac gac gcc cgc cgc gtc atg gag acc 288
 Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
 85 90 95

gtc cgt acc cct gag cgt gcg aaa gcc gaa atg gat gaa atc atc gcg 336
 Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
 100 105 110

gtg cac tct gaa aac aat gcg gca ctt cct ggt gtt aag cag tct tcg 384
 Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
 115 120 125

ggc cag gct tca ggc cag gtt tct agc aag cac acc cac atg tcc atc 432
 Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
 130 135 140

ggc gaa gtc ctc agc aac aaa tgg ctg gtt cgt ctg ctc atc gcc ggc 480
 Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
 145 150 155 160

atc ggt gtt gca gtt gcc cag cag ctc acc ggc atc aac gcc atc atg 528
 Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
 165 170 175

tac tac gga acc cgc gtc ctc gag gaa tcc ggc atg agc gca gaa atg 576
 Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
 180 185 190

gct gtg gtt gcc aac att gct ttc ggt gcc gtt gcc gtc atc ggt gga 624
 Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
 195 200 205

ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc 672
 Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
 210 215 220

atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg 711
 Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu
 225 230 235

<210> 240

<211> 237

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
 1 5 10 15

Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
 20 25 30

Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val
 35 40 45

Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
 50 55 60

Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp

65 70 75 80

Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
85 90 95

Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
100 105 110

Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
115 120 125

Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
130 135 140

Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
145 150 155 160

Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
165 170 175

Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
180 185 190

Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
195 200 205

Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
210 215 220

Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu
225 230 235

<210> 241
<211> 725
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (3)..(695)
<223> RXS03220

<400> 241
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Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
1 5 10 15

ctg gta ggt atc gga ttg ggt gtc gca cag cag ctg acc ggc atc aac 98
Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn
20 25 30

tcc atc atg tac tac ggc cag gtt gtt ctc att gag gct ggt ttc tcc 146
Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser
35 40 45

gag aat gca gct ctg atc gcc aac gtg gcg cca gga gtg atc gca gtt 194
Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val
50 55 60

gtc ggt gca ttc atc gca ctg tgg atg atg gat ggt atc aac cgc cgt 242

Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg
 65 70 75 80
 acc acc ctc att acc ggt tat tct ctc acc acc att agc cac gta ttg 290
 Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu
 85 90 95
 atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct ctt cgc ccc 338
 Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro
 100 105 110
 tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc atg cag acc 386
 Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser Met Gln Thr
 115 120 125
 ttc ctc aac gta gct acc tgg gtt atg ctc tct gag ctc ttc ccg ctg 434
 Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu
 130 135 140
 gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc ctc tgg atc 482
 Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile
 145 150 155 160
 gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg gaa gca gta 530
 Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val
 165 170 175
 gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt gtg gtt gcc 578
 Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala
 180 185 190
 ttg atc ttc atc tac acc cag gtt cct gaa act cgt gga cgt acc ttg 626
 Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu
 195 200 205
 gag gag att gat gag gat gtt act tcc ggt gtc att ttc aac aag gac 674
 Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp
 210 215 220
 atc cga aaa gga aag gtg cac taaaaaccca gacactgcat agataacacg 725
 Ile Arg Lys Gly Lys Val His
 225 230

<210> 242

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
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 Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn
 20 25 30
 Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser
 35 40 45
 Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val
 50 55 60

Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg
 65 70 75 80
 Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu
 85 90 95
 Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro
 100 105 110
 Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser Met Gln Thr
 115 120 125
 Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu
 130 135 140
 Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile
 145 150 155 160
 Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val
 165 170 175
 Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala
 180 185 190
 Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu
 195 200 205
 Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp
 210 215 220
 Ile Arg Lys Gly Lys Val His
 225 230

<210> 243

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> FRXA02762

<400> 243

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 ggatccatgc agaccttctt caacggttagc tacctggggtt atg ctc tct gag ctc 115
 Met Leu Ser Glu Leu
 1 5
 ttc ccg ctg gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc 163
 Phe Pro Leu Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe
 10 15 20
 ctc tgg atc gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg 211
 Leu Trp Ile Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met
 25 30 35
 gaa gca gta gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt 259

Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser
 10 15 20

cac gta ttg atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct 211
 His Val Leu Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro
 25 30 35

ctt cgc ccc tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc 259
 Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser
 40 45 50

atg cag acc ttc ctc aac ggt agc tac ctg ggt tat gct ctc 301
 Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly Tyr Ala Leu
 55 60 65

tgagctcttc ccgctggcaa tgc 324

<210> 246
 <211> 67
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 246
 Met Met Asp Gly Ile Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser
 1 5 10 15

Leu Thr Thr Ile Ser His Val Leu Ile Gly Ile Ala Ser Val Ala Phe
 20 25 30

Pro Val Gly Asp Pro Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val
 35 40 45

Val Phe Val Gly Ser Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly
 50 55 60

Tyr Ala Leu
 65

<210> 247
 <211> 1242
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1219)
 <223> RXA00123

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tagtagaaat tgctgtccag aactgttgaa ggagttgaaa atg cca aag aat tac 115
 Met Pro Lys Asn Tyr
 1 5

gac atc aac ggg gcg atc cgc aga cgg gat atg ctc aga cgt cgg tac 163
 Asp Ile Asn Gly Ala Ile Arg Arg Arg Asp Met Leu Arg Arg Arg Tyr
 10 15 20

[illegible]

130 135 140
 Ala Ile Ala Ile Leu Cys Gln Asp Asn Gln Trp Ile Asp Gly Thr Ser
 145 150 155 160
 Ala Ala Ser Phe Ser Asn Pro Glu Glu Ile Asp Lys Arg Ile Lys Thr
 165 170 175
 Leu Leu Ala Asp Ala Glu Leu Leu Ser Ser Gly Pro Arg Ala Ala Ala
 180 185 190
 Tyr Arg Leu Leu Asp Ala Ile Val Asp Gly Phe Ser Pro Val Leu Arg
 195 200 205
 Gly Ile Ala Ile Asp Gln Glu Gln Ile Glu Arg Gln Val Phe Ser Gly
 210 215 220
 Asp Ala Ala Val Ala Glu Arg Ile Tyr Asn Leu Ser Gln Glu Ile Ile
 225 230 235 240
 Asp Met Gln His Thr Thr Ser Ser Val Thr Glu Val Val Gln Arg Leu
 245 250 255
 Asn Lys Asp Phe Ile Arg Ser Gly Met Ser Glu Glu Leu Arg Ala Tyr
 260 265 270
 Leu Asp Asp Val Ala Asp His Leu Thr Arg Asp Asn Thr Arg Val Ser
 275 280 285
 Glu Tyr Arg Glu Ser Leu Ser Gln Ile Leu Asn Val Asn Ala Thr Leu
 290 295 300
 Val Ala Gln Arg Gln Asn Glu Asp Met Lys Lys Ile Ser Gly Trp Ala
 305 310 315 320
 Ala Ile Ile Phe Ala Pro Thr Leu Val Ser Ser Ile Tyr Gly Met Asn
 325 330 335
 Phe Asp Ile Met Pro Glu Leu His Trp Ala Phe Gly Tyr Pro Leu Ala
 340 345 350
 Leu Leu Ala Met Leu Gly Phe Thr Leu Leu Leu Tyr Trp Ile Phe Lys
 355 360 365
 Arg Ser Lys Trp Met
 370

<210> 249

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXA02441

<400> 249

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aaaaacttca tttgaaaatg ataaccgtta tcattaagga atg gca gaa ctc agc																115
Met Ala Glu Leu Ser																
1																
gtc cgg aat ctc aca tgc aca tac ggc aat cac atc gcg ctc aac aac																163
Val Arg Asn Leu Thr Cys Thr Tyr Gly Asn His Ile Ala Leu Asn Asn																
10 15 20																
atc acg gca cgc ttc cca acc gga aaa ata act gcc ctc atc ggc agc																211
Ile Thr Ala Arg Phe Pro Thr Gly Lys Ile Thr Ala Leu Ile Gly Ser																
25 30 35																
aac ggc tcc gga aaa tcc aca ctg ttg gaa act ttg gcg ggc atg ctg																259
Asn Gly Ser Gly Lys Ser Thr Leu Leu Glu Thr Leu Ala Gly Met Leu																
40 45 50																
gca ccc cgc agc gga agc att aac aac ctt gtg cca gaa atc gcg ttc																307
Ala Pro Arg Ser Gly Ser Ile Asn Asn Leu Val Pro Glu Ile Ala Phe																
55 60 65																
gtc ccc caa cgc agc cac gtc tcc cat aat ttg ccc atc acg atc aga																355
Val Pro Gln Arg Ser His Val Ser His Asn Leu Pro Ile Thr Ile Arg																
70 75 80 85																
caa aca gtc agc atg ggg cga tgg tca gcc aag aaa aac tgg caa cga																403
Gln Thr Val Ser Met Gly Arg Trp Ser Ala Lys Lys Asn Trp Gln Arg																
90 95 100																
ctc act gcc gca gat tgc aac atc gtg gac agc tgc ctc gac cgg ctc																451
Leu Thr Ala Ala Asp Cys Asn Ile Val Asp Ser Cys Leu Asp Arg Leu																
105 110 115																
gaa atc tcc ggc ctc gcc gac cgc ccc ctc ggc gaa gta tca ggc ggg																499
Glu Ile Ser Gly Leu Ala Asp Arg Pro Leu Gly Glu Val Ser Gly Gly																
120 125 130																
cag cgc caa cgc gcc ctc ata gcg caa ggt tta gcg caa cag gcg ccc																547
Gln Arg Gln Arg Ala Leu Ile Ala Gln Gly Leu Ala Gln Gln Ala Pro																
135 140 145																
tta ttg ctt ctc gac gaa ccc ctc gcc gcc gtg gac tcc cac gcg gca																595
Leu Leu Leu Leu Asp Glu Pro Leu Ala Ala Val Asp Ser His Ala Ala																
150 155 160 165																
agt ctt atc gaa gat gtc att aac caa caa cgc aac caa gga acc aca																643
Ser Leu Ile Glu Asp Val Ile Asn Gln Gln Arg Asn Gln Gly Thr Thr																
170 175 180																
att att ctt gcg act cac gat ctt gat caa gca cat caa gca gat cag																691
Ile Ile Leu Ala Thr His Asp Leu Asp Gln Ala His Gln Ala Asp Gln																
185 190 195																
att atc gcc ttg gaa aaa gga atc ata aag cca cag cgc aaa gcc act																739
Ile Ile Ala Leu Glu Lys Gly Ile Ile Lys Pro Gln Arg Lys Ala Thr																
200 205 210																
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Glu Ser Ile Lys Lys Arg																
215																

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 <213> Corynebacterium glutamicum

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 Ala Leu Ile Gly Ser Asn Gly Ser Gly Lys Ser Thr Leu Leu Glu Thr
 35 40 45
 Leu Ala Gly Met Leu Ala Pro Arg Ser Gly Ser Ile Asn Asn Leu Val
 50 55 60
 Pro Glu Ile Ala Phe Val Pro Gln Arg Ser His Val Ser His Asn Leu
 65 70 75 80
 Pro Ile Thr Ile Arg Gln Thr Val Ser Met Gly Arg Trp Ser Ala Lys
 85 90 95
 Lys Asn Trp Gln Arg Leu Thr Ala Ala Asp Cys Asn Ile Val Asp Ser
 100 105 110
 Cys Leu Asp Arg Leu Glu Ile Ser Gly Leu Ala Asp Arg Pro Leu Gly
 115 120 125
 Glu Val Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Gln Gly Leu
 130 135 140
 Ala Gln Gln Ala Pro Leu Leu Leu Leu Asp Glu Pro Leu Ala Ala Val
 145 150 155 160
 Asp Ser His Ala Ala Ser Leu Ile Glu Asp Val Ile Asn Gln Gln Arg
 165 170 175
 Asn Gln Gly Thr Thr Ile Ile Leu Ala Thr His Asp Leu Asp Gln Ala
 180 185 190
 His Gln Ala Asp Gln Ile Ile Ala Leu Glu Lys Gly Ile Ile Lys Pro
 195 200 205
 Gln Arg Lys Ala Thr Glu Ser Ile Lys Lys Arg
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 <223> RXN02442

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				Met	Lys	Phe	Phe	Thr								
				1				5								
gac	gcc	ctc	ata	gtg	cct	ttt	gac	gtt	tca	ttc	atc	tcc	cgc	gcc	ctg	163
Asp	Ala	Leu	Ile	Val	Pro	Phe	Asp	Val	Ser	Phe	Ile	Ser	Arg	Ala	Leu	
				10				15						20		
gtc	gcc	gga	tgc	ctg	gcc	gca	att	tta	tgc	tca	ctc	att	gga	acg	tgg	211
Val	Ala	Gly	Cys	Leu	Ala	Ala	Ile	Leu	Cys	Ser	Leu	Ile	Gly	Thr	Trp	
			25					30					35			
gtt	att	ttg	cgc	agg	cta	acc	ttt	ttc	ggc	gac	gct	atg	tcg	cac	ggc	259
Val	Ile	Leu	Arg	Arg	Leu	Thr	Phe	Phe	Gly	Asp	Ala	Met	Ser	His	Gly	
		40					45					50				
ttg	ctc	ccc	gga	gta	gcc	acg	gca	tca	cta	ttg	ggc	gga	aat	ctc	atg	307
Leu	Leu	Pro	Gly	Val	Ala	Thr	Ala	Ser	Leu	Leu	Gly	Gly	Asn	Leu	Met	
	55					60					65					
ttc	ggc	gca	gca	atc	agc	gca	tta	atc	atg	tca	gcc	gga	gtg	gtg	tgg	355
Phe	Gly	Ala	Ala	Ile	Ser	Ala	Leu	Ile	Met	Ser	Ala	Gly	Val	Val	Trp	
	70				75				80						85	
acc	agc	aga	aaa	tcc	agc	ctc	tcc	caa	gac	gtc	agc	att	ggc	ctg	caa	403
Thr	Ser	Arg	Lys	Ser	Ser	Leu	Ser	Gln	Asp	Val	Ser	Ile	Gly	Leu	Gln	
				90					95					100		
ttt	att	acc	atg	ctt	tcc	ctc	ggc	gtg	gtt	att	gtg	tcc	cac	tcc	gat	451
Phe	Ile	Thr	Met	Leu	Ser	Leu	Gly	Val	Val	Ile	Val	Ser	His	Ser	Asp	
			105					110					115			
tcc	cac	gcc	gta	gac	ctc	acc	agt	ttc	ctt	ttt	gga	gac	att	ctt	ggc	499
Ser	His	Ala	Val	Asp	Leu	Thr	Ser	Phe	Leu	Phe	Gly	Asp	Ile	Leu	Gly	
		120					125					130				
gtg	cga	ccc	tcg	gat	ata	ttc	atc	atc	gcc	att	gca	aca	gtg	ttg	ggc	547
Val	Arg	Pro	Ser	Asp	Ile	Phe	Ile	Ile	Ala	Ile	Ala	Thr	Val	Leu	Gly	
	135					140					145					
gga	ttg	act	att	ttt	ctc	ttc	cac	cga	cag	ttc	act	gca	ctc	gct	ttc	595
Gly	Leu	Thr	Ile	Phe	Leu	Phe	His	Arg	Gln	Phe	Thr	Ala	Leu	Ala	Phe	
150					155				160						165	
gac	gag	cgt	aaa	gct	cac	acc	tta	gga	ctc	aat	ccc	cgc	ttt	gca	cac	643
Asp	Glu	Arg	Lys	Ala	His	Thr	Leu	Gly	Leu	Asn	Pro	Arg	Phe	Ala	His	
				170				175						180		
cta	ctc	atg	ctg	gca	ctg	atc	gca	tta	gct	acg	gtg	gtg	tcg	ttt	cag	691
Leu	Leu	Met	Leu	Ala	Leu	Ile	Ala	Leu	Ala	Thr	Val	Val	Ser	Phe	Gln	
			185					190					195			
gtg	gtg	gga	acg	ctt	tta	gtg	ttt	gga	ctt	ctc	att	ggc	cgc	ccc	gcc	739
Val	Val	Gly	Thr	Leu	Leu	Val	Phe	G								

agg tta aac ttc acc gcg tgatactgaa agacattttc aat 972
Arg Leu Asn Phe Thr Ala
280

<213> Corynebacterium glutamicum

Val Val Ser Phe Gln Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu
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Ile Gly Pro Pro Ala Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser
 210 215 220

Ile Ser Leu Ile Met Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile
 225 230 235 240

Tyr Leu Gly Leu Leu Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala
 245 250 255

Thr Ile Thr Leu Leu Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr
 260 265 270

Lys Ser Ala Ile Ser Arg Leu Asn Phe Thr Ala
 275 280

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 Met Lys Phe Phe Thr
 1 5

gac gcc ctc ata gtg cct ttt gac gtt tca ttc atc tcc cgc gcc ctg 163
 Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe Ile Ser Arg Ala Leu
 10 15 20

gtc gcc gga tgc ctg gcc gca att tta tgc tca ctc att gga acg tgg 211
 Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser Leu Ile Gly Thr Trp
 25 30 35

gtt att ttg cgc agg cta acc ttt ttc ggc gac gct atg tcg cac ggc 259
 Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp Ala Met Ser His Gly
 40 45 50

ttg ctc ccc gga gta gcc acg gca tca cta ttg ggc gga aat ctc atg 307
 Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu Gly Gly Asn Leu Met
 55 60 65

ttc ggc gca gca atc agc gca tta atc atg tca gcc gga gtg gtg tgg 355
 Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser Ala Gly Val Val Trp
 70 75 80 85

acc agc aga aaa tcc agc ctc tcc caa gac gtc agc att ggc ctg caa 403
 Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val Ser Ile Gly Leu Gln
 90 95 100

ttt att acc atg ctt tcc ctc ggc gtg gtt att gtg tcc cac tcc gat 451
 Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile Val Ser His Ser Asp
 105 110 115

tcc cac gcc gta gac ctc acc agt ttc ctt ttt gga gac att ctt ggc 499
 Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe Gly Asp Ile Leu Gly
 120 125 130

gtg cga ccc tcg gat ata ttc atc atc gcc att gca aca gtg ttg ggt 547
 Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile Ala Thr Val Leu Gly
 135 140 145

gga ttg act att ttt ctc ttc cac cga cag ttc act gca ctc gct ttc 595
 Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe Thr Ala Leu Ala Phe
 150 155 160 165

gac gag cgt aaa gct cac acc tta gga ctc aat ccc cgc ttt gca cac 643
 Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn Pro Arg Phe Ala His
 170 175 180

cta ctc atg ctg gca ctg atc gca tta gct acg gtg gtg tcg ttt cag 691
 Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr Val Val Ser Phe Gln
 185 190 195

gtg gtg gga acg ctt tta gtg ttt gga ctt ctc att ggt ccg ccc gcc 739
 Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu Ile Gly Pro Pro Ala
 200 205 210

acg gct gca ctt tta gtg caa gac aaa gca agt att tca ctg atc atg 787
 Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser Ile Ser Leu Ile Met
 215 220 225

atc gtc gcg tcg ctt ctt gga tgc gcg gaa att tac ctc ggg ctt tta 835
 Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile Tyr Leu Gly Leu Leu
 230 235 240 245

atc agc tgg cac gca agc act gcc gcg gga gcc act atc act ttg tta 883
 Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala Thr Ile Thr Leu Leu
 250 255 260

agt gct gcg ata ttt ttt gcc acc tta ttg aca aag agt gcc att agt 931
 Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr Lys Ser Ala Ile Ser
 265 270 275

agg tta aac ttc acc gcg tgatactgaa agacattttc aat 972
 Arg Leu Asn Phe Thr Ala
 280

<210> 254

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Met Lys Phe Phe Thr Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe
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Ile Ser Arg Ala Leu Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser
20 25 30

Leu Ile Gly Thr Trp Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp
35 40 45

Ala Met Ser His Gly Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu
50 55 60

Gly Gly Asn Leu Met Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser
65 70 75 80

Ala Gly Val Val Trp Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val
85 90 95

Ser Ile Gly Leu Gln Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile
100 105 110

Val Ser His Ser Asp Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe
115 120 125

Gly Asp Ile Leu Gly Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile
130 135 140

Ala Thr Val Leu Gly Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe
145 150 155 160

Thr Ala Leu Ala Phe Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn
165 170 175

Pro Arg Phe Ala His Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr
180 185 190

Val Val Ser Phe Gln Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu
195 200 205

Ile Gly Pro Pro Ala Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser
210 215 220

Ile Ser Leu Ile Met Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile
225 230 235 240

Tyr Leu Gly Leu Leu Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala
245 250 255

Thr Ile Thr Leu Leu Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr
260 265 270

Lys Ser Ala Ile Ser Arg Leu Asn Phe Thr Ala
275 280

<210> 255

<211> 1431

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1408)

<223> RXA01756

<400> 255

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gcgcctgaaa tcgggcttgt tgaggggaga ggtgtgtgac atg aaa gag ttg gaa 115
Met Lys Glu Leu Glu

	1	5	
ctg ggc gag gcg agg gac gtc gct gca acg ttg gaa gcg atg ccg atc			163
Leu Gly Glu Ala Arg Asp Val Ala Ala Thr Leu Glu Ala Met Pro Ile			
	10	20	
cag gag gtt att gat cag gtt gag cga act tct ata act aaa ggt gcg			211
Gln Glu Val Ile Asp Gln Val Glu Arg Thr Ser Ile Thr Lys Gly Ala			
	25	35	
gta ctg ctg cgt ctg ctc agt aaa gat cga tcg ttg ttg gtc ttc gat			259
Val Leu Leu Arg Leu Leu Ser Lys Asp Arg Ser Leu Leu Val Phe Asp			
	40	50	
gct ctt ggt ccg cga ctc cag gct gat ctc att ggt gct ttt cag gat			307
Ala Leu Gly Pro Arg Leu Gln Ala Asp Leu Ile Gly Ala Phe Gln Asp			
	55	65	
gcg gaa gtg ctg gat tat ttc gct gac ctt gac cct gat gac cgc gtt			355
Ala Glu Val Leu Asp Tyr Phe Ala Asp Leu Asp Pro Asp Asp Arg Val			
	70	80	85
tca ctg ctt gat gag ctg ccg gcg tcg atc gct gac gag ttg ctt cgc			403
Ser Leu Leu Asp Glu Leu Pro Ala Ser Ile Ala Asp Glu Leu Leu Arg			
	90	95	100
agt ctc gat ccg cag gaa aag cag gtc acg gag ctg gtc ttg ggt tac			451
Ser Leu Asp Pro Gln Glu Lys Gln Val Thr Glu Leu Val Leu Gly Tyr			
	105	110	115
gca aag ggg tcg gtt gga cgt tgg atg tcg ccc cag gtt tta ttg ctt			499
Ala Lys Gly Ser Val Gly Arg Trp Met Ser Pro Gln Val Leu Leu Leu			
	120	125	130
ttc gac gac atg tcc gtc gcc gaa gtc tta gat ttt gtg cgc aat cat			547
Phe Asp Asp Met Ser Val Ala Glu Val Leu Asp Phe Val Arg Asn His			
	135	140	145
gct gct gag gct gag acg att tat gcc tta cct att gtg aac cgt gct			595
Ala Ala Glu Ala Glu Thr Ile Tyr Ala Leu Pro Ile Val Asn Arg Ala			
	150	155	160
cgc caa gtg atg ggc gtg gtg tcg ttg cga aag ctg ttc atc gca gat			643
Arg Gln Val Met Gly Val Val Ser Leu Arg Lys Leu Phe Ile Ala Asp			
	170	175	180
ccc act cta aaa gtc tcg gaa atc atg gtg cgt cct gtt tcg gtg ttg			691
Pro Thr Leu Lys Val Ser Glu Ile Met Val Arg Pro Val Ser Val Leu			
	185	190	195
gcg tcc gcg gat att gaa gaa acc gcc cgc tgg ttc cta cag ttg gac			739
Ala Ser Ala Asp Ile Glu Glu Thr Ala Arg Trp Phe Leu Gln Leu Asp			
	200	205	210
ctc gtt gcg atg ccc gtt gtg gat gaa tcg aac atg ctc tta gga gtg			787
Leu Val Ala Met Pro Val Val Asp Glu Ser Asn Met Leu Leu Gly Val			
	215	220	225
ctg acc ttc gat gat gcg caa gac atc gtg gag caa gcc gac tct gag			835
Leu Thr Phe Asp Asp Ala Gln Asp Ile Val Glu Gln Ala Asp Ser Glu			
	230	235	240
			245

gac tcc gct cgc agt ggt ggt tcg gaa cct ctc cag cag ccg tat cta 883
 Asp Ser Ala Arg Ser Gly Gly Ser Glu Pro Leu Gln Gln Pro Tyr Leu
 250 255 260

tcc acg ccg att cgg aaa ctg gtg aag tcc cgc atc gta tgg ctt ctg 931
 Ser Thr Pro Ile Arg Lys Leu Val Lys Ser Arg Ile Val Trp Leu Leu
 265 270 275

gtt ttg gca gtg tca gca att ttg acg gtt caa gtt ctt gat att ttc 979
 Val Leu Ala Val Ser Ala Ile Leu Thr Val Gln Val Leu Asp Ile Phe
 280 285 290

gaa gcc acc ttg gtt gaa gcc gtg gta ctg gca ttg ttc att cct ttg 1027
 Glu Ala Thr Leu Val Glu Ala Val Val Leu Ala Leu Phe Ile Pro Leu
 295 300 305

ctc act ggt act ggc gga aac acc gga aac caa gct gca aca acc gtg 1075
 Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln Ala Ala Thr Thr Val
 310 315 320 325

acc cgt gcg ctc gca ttg ggt gac gtc cga aaa tca gat gtc ttc cgc 1123
 Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys Ser Asp Val Phe Arg
 330 335 340

gtc ttg ggc aga gaa atc cga gtc ggc ctc atg ctc ggg gca ttg ttg 1171
 Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met Leu Gly Ala Leu Leu
 345 350 355

ggt gcc gtt gga ttt gtg atc gca tcg ctt gtt tac ggc atg ccc gta 1219
 Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val Tyr Gly Met Pro Val
 360 365 370

ggc act gtc atc ggt ctg aca ttg ttg gcg gtg tgc acg atg gcc gca 1267
 Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val Cys Thr Met Ala Ala
 375 380 385

tca gtt ggc gga gta atg cca att att gcc aag gcg atc gga gcg gac 1315
 Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys Ala Ile Gly Ala Asp
 390 395 400 405

cca gcg gtg ttc tct aat cct ttt att tca acc ttc tgt gat gca aca 1363
 Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr Phe Cys Asp Ala Thr
 410 415 420

ggt ttg atc atc tac ttt gca att gcc aag ttg gtg ctc gga atc 1408
 Gly Leu Ile Ile Tyr Phe Ala Ile Ala Lys Leu Val Leu Gly Ile
 425 430 435

taaaagattt ttgcttttcg acg 1431

<210> 256

<211> 436

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

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Glu Ala Met Pro Ile Gln Glu Val Ile Asp Gln Val Glu Arg Thr Ser
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 Ile Thr Lys Gly Ala Val Leu Leu Arg Leu Leu Ser Lys Asp Arg Ser
 35 40 45
 Leu Leu Val Phe Asp Ala Leu Gly Pro Arg Leu Gln Ala Asp Leu Ile
 50 55 60
 Gly Ala Phe Gln Asp Ala Glu Val Leu Asp Tyr Phe Ala Asp Leu Asp
 65 70 75 80
 Pro Asp Asp Arg Val Ser Leu Leu Asp Glu Leu Pro Ala Ser Ile Ala
 85 90 95
 Asp Glu Leu Leu Arg Ser Leu Asp Pro Gln Glu Lys Gln Val Thr Glu
 100 105 110
 Leu Val Leu Gly Tyr Ala Lys Gly Ser Val Gly Arg Trp Met Ser Pro
 115 120 125
 Gln Val Leu Leu Leu Phe Asp Asp Met Ser Val Ala Glu Val Leu Asp
 130 135 140
 Phe Val Arg Asn His Ala Ala Glu Ala Glu Thr Ile Tyr Ala Leu Pro
 145 150 155 160
 Ile Val Asn Arg Ala Arg Gln Val Met Gly Val Val Ser Leu Arg Lys
 165 170 175
 Leu Phe Ile Ala Asp Pro Thr Leu Lys Val Ser Glu Ile Met Val Arg
 180 185 190
 Pro Val Ser Val Leu Ala Ser Ala Asp Ile Glu Glu Thr Ala Arg Trp
 195 200 205
 Phe Leu Gln Leu Asp Leu Val Ala Met Pro Val Val Asp Glu Ser Asn
 210 215 220
 Met Leu Leu Gly Val Leu Thr Phe Asp Asp Ala Gln Asp Ile Val Glu
 225 230 235 240
 Gln Ala Asp Ser Glu Asp Ser Ala Arg Ser Gly Gly Ser Glu Pro Leu
 245 250 255
 Gln Gln Pro Tyr Leu Ser Thr Pro Ile Arg Lys Leu Val Lys Ser Arg
 260 265 270
 Ile Val Trp Leu Leu Val Leu Ala Val Ser Ala Ile Leu Thr Val Gln
 275 280 285
 Val Leu Asp Ile Phe Glu Ala Thr Leu Val Glu Ala Val Val Leu Ala
 290 295 300
 Leu Phe Ile Pro Leu Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln
 305 310 315 320
 Ala Ala Thr Thr Val Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys
 325 330 335
 Ser Asp Val Phe Arg Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met

340 345 350

Leu Gly Ala Leu Leu Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val
355 360 365

Tyr Gly Met Pro Val Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val
370 375 380

Cys Thr Met Ala Ala Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys
385 390 395 400

Ala Ile Gly Ala Asp Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr
405 410 415

Phe Cys Asp Ala Thr Gly Leu Ile Ile Tyr Phe Ala Ile Ala Lys Leu
420 425 430

Val Leu Gly Ile
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<210> 257
<211> 1142
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(1119)
<223> RXA02068

<400> 257

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act ttg gtt acc ggt tct gta tca ctt cga acc ttt cgc gtg cgc acc	96
Thr Leu Val Thr Gly Ser Val Ser Leu Arg Thr Phe Arg Val Arg Thr	
20 25 30	
ggt gaa ttg cag gtc atg ggc gat att gtg ggt gca aaa gta cat acc	144
Gly Glu Leu Gln Val Met Gly Asp Ile Val Gly Ala Lys Val His Thr	
35 40 45	
gat gat cca gag ctg caa caa ttc cac ggt cgc gcg gta gaa atc gcc	192
Asp Asp Pro Glu Leu Gln Gln Phe His Gly Arg Ala Val Glu Ile Ala	
50 55 60	
gat gtg gag ctg gag tta tcg cgc act cgc gat tgg atc atc acg cgc	240
Asp Val Glu Leu Glu Leu Ser Arg Thr Arg Asp Trp Ile Ile Thr Arg	
65 70 75 80	
gtg gcg gtg ctg ggt gag cgc cct aaa ttt ggc cgg cgc cca gtg ctg	288
Val Ala Val Leu Gly Glu Arg Pro Lys Phe Gly Arg Arg Pro Val Leu	
85 90 95	
cac aca gtg ccg tgg agt cat atc cac ggc atc acc gca ggt ggt gtc	336
His Thr Val Pro Trp Ser His Ile His Gly Ile Thr Ala Gly Gly Val	
100 105 110	
ggc gag tcc aat cac acc gcc gaa ctc atc gca ggg ttt gag gat atg	384

Gly	Glu	Ser	Asn	His	Thr	Ala	Glu	Leu	Ile	Ala	Gly	Phe	Glu	Asp	Met	
		115					120					125				
agg	cct	gcg	gac	gtc	gca	aag	cag	ctt	tat	cag	ctg	cct	acg	gct	cag	432
Arg	Pro	Ala	Asp	Val	Ala	Lys	Gln	Leu	Tyr	Gln	Leu	Pro	Thr	Ala	Gln	
	130					135					140					
cgt	acc	gaa	gtg	acg	gaa	gag	ctt	gac	gac	gaa	aag	ctg	gcg	gat	atc	480
Arg	Thr	Glu	Val	Thr	Glu	Glu	Leu	Asp	Asp	Glu	Lys	Leu	Ala	Asp	Ile	
145					150					155					160	
ctg	cag	gaa	ttg	tcc	gag	gac	cgc	caa	gcc	gag	ttg	att	gaa	gaa	tta	528
Leu	Gln	Glu	Leu	Ser	Glu	Asp	Arg	Gln	Ala	Glu	Leu	Ile	Glu	Glu	Leu	
				165				170							175	
gac	atc	gaa	cgt	gcc	gcg	gac	att	ctg	gag	gaa	atg	gat	cca	gat	gat	576
Asp	Ile	Glu	Arg	Ala	Ala	Asp	Ile	Leu	Glu	Glu	Met	Asp	Pro	Asp	Asp	
			180					185					190			
gct	gca	gac	ttg	ttg	ggt	gag	ctg	cct	gat	gac	aaa	gct	gat	gtg	ttg	624
Ala	Ala	Asp	Leu	Leu	Gly	Glu	Leu	Pro	Asp	Asp	Lys	Ala	Asp	Val	Leu	
		195					200					205				
ttg	gat	ctg	atg	gac	cct	gag	gaa	tct	gcg	ccg	gtg	cgt	cgt	ttg	atg	672
Leu	Asp	Leu	Met	Asp	Pro	Glu	Glu	Ser	Ala	Pro	Val	Arg	Arg	Leu	Met	
	210					215					220					
gat	ttc	tcc	ccg	gac	acc	gtt	ggt	gcg	ctg	atg	act	cct	gag	cca	tta	720
Asp	Phe	Ser	Pro	Asp	Thr	Val	Gly	Ala	Leu	Met	Thr	Pro	Glu	Pro	Leu	
225					230				235						240	
att	atg	gat	cct	tcc	acc	aca	gtc	gct	gaa	gcg	ttg	gcg	atg	gcc	aga	768
Ile	Met	Asp	Pro	Ser	Thr	Thr	Val	Ala	Glu	Ala	Leu	Ala	Met	Ala	Arg	
				245					250					255		
aac	ccc	gac	ctt	cct	act	tct	ttg	gca	tgc	ttg	atc	ttt	gtg	gtg	cgc	816
Asn	Pro	Asp	Leu	Pro	Thr	Ser	Leu	Ala	Ser	Leu	Ile	Phe	Val	Val	Arg	
			260					265					270			
cca	ccc	acg	gcc	acg	cct	act	gga	aaa	tac	ctc	ggc	tgc	gtg	cat	ctg	864
Pro	Pro	Thr	Ala	Thr	Pro	Thr	Gly	Lys	Tyr	Leu	Gly	Cys	Val	His	Leu	
		275					280					285				
cag	aaa	ctg	ctt	cgg	gag	cct	cca	tca	agt	ttg	att	ggt	ggc	atc	ctc	912
Gln	Lys	Leu	Leu	Arg	Glu	Pro	Pro	Ser	Ser	Leu	Ile	Gly	Gly	Ile	Leu	
	290				295						300					
gac	ccc	gat	ctg	cca	ccg	ctc	tac	gct	gat	gat	tct	caa	gaa	acc	gca	960
Asp	Pro	Asp	Leu	Pro	Pro	Leu	Tyr	Ala	Asp	Asp	Ser	Gln	Glu	Thr	Ala	
305					310				315						320	
gct	cga	ttc	ttt	gcc	acc	tac	aac	ttg	gtg	tgc	ggc	ccc	gtc	ttg	gat	1008
Ala	Arg	Phe	Phe	Ala	Thr	Tyr	Asn	Leu	Val	Cys	Gly	Pro	Val	Leu	Asp	
				325				330						335		
gaa	aac	cgc	cat	ctg	ctt	ggt	gcc	gta	gct	gtc	gat	gac	ttg	ctc	gac	1056
Glu	Asn	Arg	His	Leu	Leu	Gly	Ala	Val	Ala	Val	Asp	Asp	Leu	Leu	Asp	
			340				345						350			
cac	atg	ctg	cca	gaa	gac	tgg	cgc	gac	gcc	gga	atc	cga	cca	gga	aag	1104
His	Met	Leu	Pro	Glu	Asp	Trp	Arg	Asp	Ala	Gly	Ile	Arg	Pro	Gly	Lys	

355

360

365

gag cac acc cat ggc tgatttcaac cgctctgaat tag
 Glu His Thr His Gly
 370

1142

<210> 258

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

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Thr Leu Val Thr Gly Ser Val Ser Leu Arg Thr Phe Arg Val Arg Thr
 20 25 30

Gly Glu Leu Gln Val Met Gly Asp Ile Val Gly Ala Lys Val His Thr
 35 40 45

Asp Asp Pro Glu Leu Gln Gln Phe His Gly Arg Ala Val Glu Ile Ala
 50 55 60

Asp Val Glu Leu Glu Leu Ser Arg Thr Arg Asp Trp Ile Ile Thr Arg
 65 70 75 80

Val Ala Val Leu Gly Glu Arg Pro Lys Phe Gly Arg Arg Pro Val Leu
 85 90 95

His Thr Val Pro Trp Ser His Ile His Gly Ile Thr Ala Gly Gly Val
 100 105 110

Gly Glu Ser Asn His Thr Ala Glu Leu Ile Ala Gly Phe Glu Asp Met
 115 120 125

Arg Pro Ala Asp Val Ala Lys Gln Leu Tyr Gln Leu Pro Thr Ala Gln
 130 135 140

Arg Thr Glu Val Thr Glu Glu Leu Asp Asp Glu Lys Leu Ala Asp Ile
 145 150 155 160

Leu Gln Glu Leu Ser Glu Asp Arg Gln Ala Glu Leu Ile Glu Glu Leu
 165 170 175

Asp Ile Glu Arg Ala Ala Asp Ile Leu Glu Glu Met Asp Pro Asp Asp
 180 185 190

Ala Ala Asp Leu Leu Gly Glu Leu Pro Asp Asp Lys Ala Asp Val Leu
 195 200 205

Leu Asp Leu Met Asp Pro Glu Glu Ser Ala Pro Val Arg Arg Leu Met
 210 215 220

Asp Phe Ser Pro Asp Thr Val Gly Ala Leu Met Thr Pro Glu Pro Leu
 225 230 235 240

Ile Met Asp Pro Ser Thr Thr Val Ala Glu Ala Leu Ala Met Ala Arg
 245 250 255

gca ggt gtt gtc tcc ctc gac ggc gac ggc tcc acc acc 538
Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser Thr Thr
135 140 145

<213> Corynebacterium glutamicum

Thr Thr
145

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<221> CDS
 <222> (1)..(258)
 <223> RXA02808

<400> 261

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Phe Tyr Phe Gly Ile Leu Pro Val Leu Ala Glu Ser Ala Ser His Phe	
1 5 10 15	
ggc atc gag cct gtg gaa atg gcc cgc gca tcc atc act ggc cag ccc	96
Gly Ile Glu Pro Val Glu Met Ala Arg Ala Ser Ile Thr Gly Gln Pro	
20 25 30	
gtt cac atg caa agc ccg ctg gtc cca gcg atc ctc ctg ctg gtt tcc	144
Val His Met Gln Ser Pro Leu Val Pro Ala Ile Leu Leu Leu Val Ser	
35 40 45	
ctc gcc aac gtc aac ctt ggc gac cac cac aag aag gtt ctg tgg cgc	192
Leu Ala Asn Val Asn Leu Gly Asp His His Lys Lys Val Leu Trp Arg	
50 55 60	
gcc tgc atc gtg tcc atc gcg atg ctc gcc gta gcc ctc ttc atc ggc	240
Ala Cys Ile Val Ser Ile Ala Met Leu Ala Val Ala Leu Phe Ile Gly	
65 70 75 80	
gtc gtg cca ctc agc gca taaaatagct ttctgacgcc aaa	281
Val Val Pro Leu Ser Ala	
85	

<210> 262
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 262

Phe Tyr Phe Gly Ile Leu Pro Val Leu Ala Glu Ser Ala Ser His Phe	
1 5 10 15	
Gly Ile Glu Pro Val Glu Met Ala Arg Ala Ser Ile Thr Gly Gln Pro	
20 25 30	
Val His Met Gln Ser Pro Leu Val Pro Ala Ile Leu Leu Leu Val Ser	
35 40 45	
Leu Ala Asn Val Asn Leu Gly Asp His His Lys Lys Val Leu Trp Arg	
50 55 60	
Ala Cys Ile Val Ser Ile Ala Met Leu Ala Val Ala Leu Phe Ile Gly	
65 70 75 80	
Val Val Pro Leu Ser Ala	
85	

<210> 263
 <211> 960
 <212> DNA
 <213> Corynebacterium glutamicum

<220>


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<210> 264
<211> 279
<212> PRT
<213> Corynebacterium glutamicum

<400> 264
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Leu Pro Gly Trp Leu Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile
          20          25          30
Ile Gly Pro Ile Phe Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser
          35          40          45
Trp Glu Leu Leu Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser
          50          55          60
Ile Gly Thr Ala Leu Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe
  65          70          75          80
Pro Leu Ala Leu Ala Leu His Leu Tyr Glu Arg Ser His Pro Arg Val
          85          90          95
Thr Ser Val Leu Thr Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro
          100          105          110
Val Val Ser Gly Leu Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe
          115          120          125
Leu Gly Ser Trp Leu Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr
          130          135          140
Thr Ala Val Val Phe Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile
  145          150          155          160
Ser Thr Val Thr Thr Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu
          165          170          175

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Variable	Mean	SD	Min	Max
Age	35.5	10.5	20	65
Gender	0.5	0.5	0	1
Marital Status	0.5	0.5	0	1
Education	12.5	1.5	9	16
Income	15.5	5.5	10	25
Health Status	1.5	0.5	1	2
Stress Level	3.5	1.5	1	5
Life Satisfaction	4.5	1.5	1	7
Work-Life Balance	3.5	1.5	1	5
Family Support	4.5	1.5	1	7
Community Involvement	2.5	1.5	1	5
Personal Growth	3.5	1.5	1	5
Financial Stability	3.5	1.5	1	5
Emotional Well-being	4.5	1.5	1	7
Physical Health	3.5	1.5	1	5
Social Connections	3.5	1.5	1	5
Work Satisfaction	3.5	1.5	1	5
Life Goals Achievement	3.5	1.5	1	5
Overall Quality of Life	4.5	1.5	1	7

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Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala
35 40 45

[illegible]

<210> 268
 <211> 243
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 268
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 Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr
 20 25 30
 Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly
 35 40 45
 Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser
 50 55 60
 Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro
 65 70 75 80
 Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu
 85 90 95
 Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala
 100 105 110
 Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu
 115 120 125
 Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu
 130 135 140
 Ile Ser Glu Pro Glu Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu
 145 150 155 160
 Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val
 165 170 175
 Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu
 180 185 190
 Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile
 195 200 205
 Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro
 210 215 220
 Ser Phe Ala Ser Tyr Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr
 225 230 235 240
 Thr Pro Ala

<210> 269
 <211> 852
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(829)

<223> FRXA02614

<400> 269

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acaccttccg ctaccgaaac gcataagaaa gttgctcgcc atg act gcc aca ttg 115
                               Met Thr Ala Thr Leu
                               1 5

tca ctc aaa ccc gca gcc act gtc cgt gga ttg cgc aaa tca tac gga 163
Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu Arg Lys Ser Tyr Gly
          10          15          20

act aaa gaa gtc ctc caa gga atc gac ctc acc atc aac tgc ggc gaa 211
Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr Ile Asn Cys Gly Glu
          25          30          35

gta acc gcg ctg atc gga cgc tca ggt tca gga aaa tcc acc atc ctg 259
Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly Lys Ser Thr Ile Leu
          40          45          50

cgc gtg ttg gcg ggc cta tct aaa gag cat tcc ggc tct gta gaa att 307
Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser Gly Ser Val Glu Ile
          55          60          65

tcc gga aac ccg gcc gtt gcc ttc caa gag cct cgc ctg ttg ccg tgg 355
Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro Arg Leu Leu Pro Trp
          70          75          80          85

aaa acg gtg ctc gat aat gtg acc ttt ggc ctc aac cgc act gat att 403
Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu Asn Arg Thr Asp Ile
          90          95          100

tcc tgg tca gaa gca caa gaa cgc gcc tcg gca ctg ctt gca gaa gtc 451
Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala Leu Leu Ala Glu Val
          105          110          115

aaa ctt ccc gac tcc gac gcc gcc tgg ccc ctc acg ctc tcc ggc ggc 499
Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu Thr Leu Ser Gly Gly
          120          125          130

caa gcc cag cgc gtc tcc ctt gcg cga gcg ctc atc tcc gag cca gag 547
Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu Ile Ser Glu Pro Glu
          135          140          145

ctt ttg ctt ctc gac gaa ccc ttc ggc gcc ctc gat gct ctg aca aga 595
Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg
          150          155          160          165

ctg aca gcc caa gac ctg ctg ctc aaa acc gtg aac acc cga aac ttg 643
Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val Asn Thr Arg Asn Leu
          170          175          180

gga gtt ctg ctg gtc acc cat gat gtt tcc gag gcc atc gcc ctg gcc 691
Gly Val Leu Leu Val Thr His Asp Val Ser Glu Ala Ile Ala Leu Ala
          185          190          195

gac cac gtc ctt ctt ctt gac gac ggc gcc atc aca cac agt ttg act 739

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115
 163
 211
 259
 307
 355
 403
 451
 499
 547
 595
 643
 691
 739

Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr
 200 205 210

gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac 787
 Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr
 215 220 225

acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc 829
 Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala
 230 235 240

tagaaagaaa tcatgaaatt taa 852

<210> 270
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 270
 Met Thr Ala Thr Leu Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu
 1 5 10 15

Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr
 20 25 30

Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly
 35 40 45

Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser
 50 55 60

Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro
 65 70 75 80

Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu
 85 90 95

Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala
 100 105 110

Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu
 115 120 125

Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu
 130 135 140

Ile Ser Glu Pro Glu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu
 145 150 155 160

Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val
 165 170 175

Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu
 180 185 190

Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile
 195 200 205

Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro
 210 215 220

Ser Phe Ala Ser Tyr Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr
 225 230 235 240

Thr Pro Ala

<210> 271

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXN01142

<400> 271

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ccgaggcatg gttttccaag accacgccct cctgcctga ttg acc gca cgc ggc 115
                                   Leu Thr Ala Arg Gly
                                   1 5

aac atc gac ttc ggg ctc cgc tcc gcg cgc ccc tcc ttg agc aaa acc 163
Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro Ser Leu Ser Lys Thr
                                   10 15 20

gaa cgc gcc gac atc acc cgc acc cac ctc gaa caa gta ggc ctc acc 211
Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr
                                   25 30 35

gac gcc gcc gaa cgg cgc ccc gcc cgc ctc tcc ggc ggc atg caa cag 259
Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln
                                   40 45 50

cga gtc ggc atc gca cgc gcc ttc gcc atc gac cca cca atc atg ctt 307
Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu
                                   55 60 65

ctc gac gaa ccc ttc ggc gcc ctc gac gcc ctc acc cgc cgc gaa ctc 355
Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu
                                   70 75 80 85

cag ctc caa cta ctc aac att tgg gaa gcc tcc cgc cgc acc gtc gtc 403
Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val
                                   90 95 100

atg gtc acc cac gac gtc gac gag gcc atc ctg ctc tcc gac cga gtt 451
Met Val Thr His Asp Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val
                                   105 110 115

ctc gtg atg tcc aag agc ccc gaa gcc acc atc atc acc gat att cca 499
Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro
                                   120 125 130

gtg aat ctt ccc cgc ccc aga cac gag ctg agt gaa gac gct tct gtt 547
Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val
                                   135 140 145
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gaa gcc gag acc aca gcc ctg cgt aag cgg atg ctg cat ctg ctg gag 595
 Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu
 150 155 160 165

cac tagtttctaa cacgtctttt aaa 621
 His

<210> 272

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Leu Thr Ala Arg Gly Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro
 1 5 10 15

Ser Leu Ser Lys Thr Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu
 20 25 30

Gln Val Gly Leu Thr Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser
 35 40 45

Gly Gly Met Gln Gln Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp
 50 55 60

Pro Pro Ile Met Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu
 65 70 75 80

Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser
 85 90 95

Arg Arg Thr Val Val Met Val Thr His Asp Val Asp Glu Ala Ile Leu
 100 105 110

Leu Ser Asp Arg Val Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile
 115 120 125

Ile Thr Asp Ile Pro Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser
 130 135 140

Glu Asp Ala Ser Val Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met
 145 150 155 160

Leu His Leu Leu Glu His
 165

<210> 273

<211> 443

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(420)

<223> FRXA01142

<400> 273

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Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg
 1 5 10 15
 cgc ccc gcc cgc ctc tcc gcc gcc atg caa cag cga gtc gcc atc gca 96
 Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln Arg Val Gly Ile Ala
 20 25 30
 cgc gcc ttc gcc atc gac cca cca atc atg ctt ctc gac gaa ccc ttc 144
 Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu Leu Asp Glu Pro Phe
 35 40 45
 gga gcc ctc gac gcc ctc acc cgc cgc gaa ctc cag ctc caa cta ctc 192
 Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu
 50 55 60
 aac att tgg gaa gcc tcc cgc cgc acc gtc gtc atg gtc acc cac gac 240
 Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp
 65 70 75 80
 gtc gac gag gcc atc ctg ctc tcc gac cga gtt ctc gtg atg tcc aag 288
 Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys
 85 90 95
 agc ccc gaa gcc acc atc atc acc gat att cca gtg aat ctt ccc cgc 336
 Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro Val Asn Leu Pro Arg
 100 105 110
 ccc aga cac gag ctg agt gaa gac gct tct gtt gaa gcc gag acc aca 384
 Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val Glu Ala Glu Thr Thr
 115 120 125
 gcc ctg cgt aag cgg atg ctg cat ctg ctg gag cac tagttttctaa 430
 Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu His
 130 135 140
 cacgtctttt aaa 443

<210> 274

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg
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 20 25 30
 Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu Leu Asp Glu Pro Phe
 35 40 45
 Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu
 50 55 60
 Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp
 65 70 75 80
 Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys
 85 90 95

Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr
 135 140 145

ctc gtc tca aac gca gtt gat ccc atc gcc gat ctt gag ctt cgc ctg 595
 Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu
 150 155 160 165

ctc cga cct gcc gat atg gtc gca caa ttg aca gtt gag ggc atc gat 643
 Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp
 170 175 180

gga ttc att ggg cct ggg ccg ttt aat gaa cgc gcc atc agc aat ggc 691
 Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly
 185 190 195

tcc ggc cgg att tgg ctg ctg acc aaa caa ctg tgg gac aaa cat cca 739
 Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro
 200 205 210

tgc tgc gcc gtg gcg atg gcc aaa gag tgg aaa gct gaa cac ccc acg 787
 Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr
 215 220 225

gcg gct cag ggt gtg ctt aat gcg ctg gag gaa gcc tcc gca att ttg 835
 Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu
 230 235 240 245

agc aat ccg gca caa ttt gat tcc tcg gca cgc acg ctg tcg cag gaa 883
 Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu
 250 255 260

aaa tac ctc aac cag cct gcc acg ttg ctg gat gga ccg tcg 925
 Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser
 265 270 275

taatcatcgg catcaccggc tta 948

<210> 276

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

Leu Ser Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser
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Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro
 20 25 30

Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe
 35 40 45

Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser
 50 55 60

Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met
 65 70 75 80

Leu Ser Pro Met Thr Val Ala Ile Asn Ala Gly Val Thr Asn Ala Ser
 85 90 95

Arg Pro Thr Glu Leu Ser Phe Thr Gln Asn Thr Asn Gly Gln Ala Ile
 100 105 110
 Thr Leu Ala Ser Lys His Tyr Gly Ser Val Asn Ser Ala Ala Asp Leu
 115 120 125
 Lys Gly Met Val Leu Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu
 130 135 140
 Leu Leu Arg Asp Tyr Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp
 145 150 155 160
 Leu Glu Leu Arg Leu Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr
 165 170 175
 Val Glu Gly Ile Asp Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg
 180 185 190
 Ala Ile Ser Asn Gly Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu
 195 200 205
 Trp Asp Lys His Pro Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys
 210 215 220
 Ala Glu His Pro Thr Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu
 225 230 235 240
 Ala Ser Ala Ile Leu Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg
 245 250 255
 Thr Leu Ser Gln Glu Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp
 260 265 270
 Gly Pro Ser
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<211> 424

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(424)

<223> FRXA01135

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gaacactcgg tatggcacct gatttaagga tgctgcaatc gtg aca cat atc ctc 115
 Val Thr His Ile Leu
 1 5

ttc gac agc agg cgt ttt ctg caa ctg ggc gct ttt gcg tcc ttg agc 163
 Phe Asp Ser Arg Arg Phe Leu Gln Leu Gly Ala Phe Ala Ser Leu Ser
 10 15 20

acc gca ttg gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat 211
 Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn

	25	30	35	
gaa cct gcg gat aac act ccc ctg acc att ggc tac gtg cct att gcg				259
Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala				
	40	45	50	
ggc tgc gcg ccg att gct atc gca gat gcg cta ggg ctg ttt aag aaa				307
Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys				
	55	60	65	
cac ggc gtg aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg				355
His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu				
	70	75	80	85
tgg acc gcc tat gca aca gag cag ctt gat gtt gcg cac atg ctg tgc				403
Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met Leu Ser				
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ccg atg act gtg gcg att aat				424
Pro Met Thr Val Ala Ile Asn				
	105			

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 <213> Corynebacterium glutamicum

<400> 278
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 35 40 45
 Tyr Val Pro Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu
 50 55 60
 Gly Leu Phe Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser
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 Gly Trp Ser Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val
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 Ala His Met Leu Ser Pro Met Thr Val Ala Ile Asn
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 ttg ctg tct aat atg ttc ctg ctc gcg gtg atc ggt ctg ggt ctc aac 499
 Leu Leu Ser Asn Met Phe Leu Leu Ala Val Ile Gly Leu Gly Leu Asn
 120 125 130
 gag gct gcg tac atg gcg gaa atc gtg cgc tcg ggc atc caa gcg gtg 547
 Glu Ala Ala Tyr Met Ala Glu Ile Val Arg Ser Gly Ile Gln Ala Val
 135 140 145
 cct gag ggc cag atg gag gcg tcg aaa gct ttg ggt atg aac tgg tca 595
 Pro Glu Gly Gln Met Glu Ala Ser Lys Ala Leu Gly Met Asn Trp Ser
 150 155 160 165
 atg acc atg cgt cgc acc atc ttg ccg cag gcc atg cgc atc atc att 643
 Met Thr Met Arg Arg Thr Ile Leu Pro Gln Ala Met Arg Ile Ile Ile
 170 175 180
 ccg cca acc ggc aat gaa ctg atc tcc atg ctc aag acc acc tct ctg 691
 Pro Pro Thr Gly Asn Glu Leu Ile Ser Met Leu Lys Thr Thr Ser Leu
 185 190 195
 gtt gtt gog att cct tat tct ctc gag ctg tac ggc cgc agc atg gat 739
 Val Val Ala Ile Pro Tyr Ser Leu Glu Leu Tyr Gly Arg Ser Met Asp
 200 205 210
 att gcg tac tcc ctc ttc gag cca gtt cca atg ctt ctg gtt gct gcg 787
 Ile Ala Tyr Ser Leu Phe Glu Pro Val Pro Met Leu Leu Val Ala Ala
 215 220 225
 agc tgg tac ttg gtc atc acc tct att ctt atg gtt ggt cag tac tac 835
 Ser Trp Tyr Leu Val Ile Thr Ser Ile Leu Met Val Gly Gln Tyr Tyr
 230 235 240 245
 ctg gag aag cac ttc gaa aag ggc agc acc cgc acc ctg acc gca cgt 883
 Leu Glu Lys His Phe Glu Lys Gly Ser Thr Arg Thr Leu Thr Ala Arg
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 cag ctc gct 892
 Gln Leu Ala

<210> 282

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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 Ala Leu Asn Asn Glu Ala Tyr Gly Trp Asp Thr Tyr Arg Ser Tyr Leu
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 Phe Asp Thr Arg Ile Ala Thr Ala Ala Leu His Thr Ile Ala Leu Thr
 35 40 45
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<223> RXA02663
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Val Phe Ala Thr Val Leu Val Ala Asp Ala Ile Val Phe Glu Ala Ser

				10				15				20							
ctg	tcc	ttc	atc	aac	gct	ggg	gtg	aaa	cca	cca	tca	cct	tca	tgg	ggc	211			
Leu	Ser	Phe	Ile	Asn	Ala	Gly	Val	Lys	Pro	Pro	Ser	Pro	Ser	Trp	Gly				
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aac	atc	ctt	gcc	gat	ggg	aaa	gcc	ctg	ctg	ctt	agc	ggc	gca	tgg	tgg	259			
Asn	Ile	Leu	Ala	Asp	Gly	Lys	Ala	Leu	Leu	Leu	Ser	Gly	Ala	Trp	Trp				
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cca	acc	ttc	ttc	cca	ggg	ttg	atg	atc	ctg	ctg	acc	gtt	ctc	tgc	ttg	307			
Pro	Thr	Phe	Phe	Pro	Gly	Leu	Met	Ile	Leu	Leu	Thr	Val	Leu	Cys	Leu				
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aac	atc	ctt	tct	gaa	ggc	ctc	acc	gac	acc	ctg	gcc	agc	cct	aag	cca	355			
Asn	Ile	Leu	Ser	Glu	Gly	Leu	Thr	Asp	Thr	Leu	Ala	Ser	Pro	Lys	Pro				
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Lys	Pro	Val	Ser	Ala	Ser	Ala	Lys	Lys	Ala	Leu	Lys	Lys	Glu	Glu	Ser				
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Gly	Glu	Lys	Glu	Gly	Ser	Gly	Ile	Val	Leu	Gly	His	Thr	Thr	Arg	Glu				
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gaa	gcc	aac	gcc	tca	ctg	ctc	gca	tca	ctt	gct	gcg	cta	tcc	acc	agc	499			
Glu	Ala	Asn	Ala	Ser	Leu	Leu	Ala	Ser	Leu	Ala	Ala	Leu	Ser	Thr	Ser				
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gaa	aac	aat	tcc	aat	aac	cgg	ctt	ata	ttt	gat	ggc	aac	ccc	act	cct	547			
Glu	Asn	Asn	Ser	Asn	Asn	Arg	Leu	Ile	Phe	Asp	Gly	Asn	Pro	Thr	Pro				
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ctg	ttg	gaa	gtt	cgc	gat	cta	aag	atc	tcc	ttc	ccc	aat	gct	cac	gga	595			
Leu	Leu	Glu	Val	Arg	Asp	Leu	Lys	Ile	Ser	Phe	Pro	Asn	Ala	His	Gly				
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gat	atc	aat	att	gtc	gac	ggc	gtg	aac	ttc	acc	gtc	gcc	cca	ggc	caa	643			
Asp	Ile	Asn	Ile	Val	Asp	Gly	Val	Asn	Phe	Thr	Val	Ala	Pro	Gly	Gln				
170				175				180											
acc	atg	ggg	ctt	gtc	ggg	gaa	tcc	ggc	tgt	ggg	aaa	tcg	att	acc	gca	691			
Thr	Met	Gly	Leu	Val	Gly	Glu	Ser	Gly	Cys	Gly	Lys	Ser	Ile	Thr	Ala				
185				190				195											
atg	tcg	atc	atg	ggg	ctg	ctg	cct	cca	aca	gca	aag	atc	gaa	ggc	gag	739			
Met	Ser	Ile	Met	Gly	Leu	Leu	Pro	Pro	Thr	Ala	Lys	Ile	Glu	Gly	Glu				
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atc	ctt	ttc	gac	gga	aag	aac	ctc	ctt	gat	ctg	aaa	cca	gac	gag	ctc	787			
Ile	Leu	Phe	Asp	Gly	Lys	Asn	Leu	Leu	Asp	Leu	Lys	Pro	Asp	Glu	Leu				
215				220				225											
aat	gca	ctg	cgt	gga	cat	gaa	atc	gcc	atg	atc	tac	caa	gat	gca	ctc	835			
Asn	Ala	Leu	Arg	Gly	His	Glu	Ile	Ala	Met	Ile	Tyr	Gln	Asp	Ala	Leu				
230				235				240				245							
tcc	tca	ctc	aac	cca	tcc	atg													

acc cgc cgc ggt gga aag cgc agt gcc gaa gaa ctc ctg gaa ctt gta 931
 Thr Arg Arg Gly Gly Lys Arg Ser Ala Glu Glu Leu Leu Glu Leu Val
 265 270 275

ggc ctt gat cca aag cgc acc ctg cag tcc tac ccg cat gag ctt tca 979
 Gly Leu Asp Pro Lys Arg Thr Leu Gln Ser Tyr Pro His Glu Leu Ser
 280 285 290

ggt ggc cag cgc cag cga gtt ctc atc gca atg gca ctg acc aga aac 1027
 Gly Gly Gln Arg Gln Arg Val Leu Ile Ala Met Ala Leu Thr Arg Asn
 295 300 305

cca cgc ctc ctc atc gcc gac gag cca acc acc gcg cta gac gtc act 1075
 Pro Arg Leu Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Val Thr
 310 315 320 325

gtt cag cag cag gtt gtc gat ctg ctt aat gaa ctg cgt gaa aag ctc 1123
 Val Gln Gln Gln Val Val Asp Leu Leu Asn Glu Leu Arg Glu Lys Leu
 330 335 340

gga ttc gcc atg atc ttt gta tcc cac gac ttg gct ctt gtc gcc cgc 1171
 Gly Phe Ala Met Ile Phe Val Ser His Asp Leu Ala Leu Val Ala Arg
 345 350 355

ctg gtg cac aag ctc acc gtc atg tac gca ggt cag gtt gtt gag caa 1219
 Leu Val His Lys Leu Thr Val Met Tyr Ala Gly Gln Val Val Glu Gln
 360 365 370

gga acc acc cgc gaa atc ctt atc gat cct cga cac gaa tac acc cgc 1267
 Gly Thr Thr Arg Glu Ile Leu Ile Asp Pro Arg His Glu Tyr Thr Arg
 375 380 385

ggt ttg ctc gga tcc gtg ctc tcc atc gaa gct ggt gtg gac cgc ctc 1315
 Gly Leu Leu Gly Ser Val Leu Ser Ile Glu Ala Gly Val Asp Arg Leu
 390 395 400 405

tac cag gtc cca ggc act gtt cca tca cca aag gaa ttc gtg gca ggc 1363
 Tyr Gln Val Pro Gly Thr Val Pro Ser Pro Lys Glu Phe Val Ala Gly
 410 415 420

gac cgc ttt gca cca cga tca gaa ttc cca gaa ctt ggc ctt gac caa 1411
 Asp Arg Phe Ala Pro Arg Ser Glu Phe Pro Glu Leu Gly Leu Asp Gln
 425 430 435

aag cca gta ctt cgc ccc atc acg ggc aca gag cat gca tac gca gca 1459
 Lys Pro Val Leu Arg Pro Ile Thr Gly Thr Glu His Ala Tyr Ala Ala
 440 445 450

acc gat gaa ctt ctt gcc gca aag gga gaa caa cga tgacctcgac 1505
 Thr Asp Glu Leu Leu Ala Ala Lys Gly Glu Gln Arg
 455 460 465

aatcgacacc agg 1518

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<211> 465

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

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			20					25					30		
Ser	Pro	Ser	Trp	Gly	Asn	Ile	Leu	Ala	Asp	Gly	Lys	Ala	Leu	Leu	Leu
		35					40					45			
Ser	Gly	Ala	Trp	Trp	Pro	Thr	Phe	Phe	Pro	Gly	Leu	Met	Ile	Leu	Leu
	50					55					60				
Thr	Val	Leu	Cys	Leu	Asn	Ile	Leu	Ser	Glu	Gly	Leu	Thr	Asp	Thr	Leu
65					70					75					80
Ala	Ser	Pro	Lys	Pro	Lys	Pro	Val	Ser	Ala	Ser	Ala	Lys	Lys	Ala	Leu
				85					90					95	
Lys	Lys	Glu	Glu	Ser	Gly	Glu	Lys	Glu	Gly	Ser	Gly	Ile	Val	Leu	Gly
			100					105					110		
His	Thr	Thr	Arg	Glu	Glu	Ala	Asn	Ala	Ser	Leu	Leu	Ala	Ser	Leu	Ala
			115				120						125		
Ala	Leu	Ser	Thr	Ser	Glu	Asn	Asn	Ser	Asn	Asn	Arg	Leu	Ile	Phe	Asp
	130					135					140				
Gly	Asn	Pro	Thr	Pro	Leu	Leu	Glu	Val	Arg	Asp	Leu	Lys	Ile	Ser	Phe
145					150					155					160
Pro	Asn	Ala	His	Gly	Asp	Ile	Asn	Ile	Val	Asp	Gly	Val	Asn	Phe	Thr
				165					170					175	
Val	Ala	Pro	Gly	Gln	Thr	Met	Gly	Leu	Val	Gly	Glu	Ser	Gly	Cys	Gly
			180					185					190		
Lys	Ser	Ile	Thr	Ala	Met	Ser	Ile	Met	Gly	Leu	Leu	Pro	Pro	Thr	Ala
		195					200					205			
Lys	Ile	Glu	Gly	Glu	Ile	Leu	Phe	Asp	Gly	Lys	Asn	Leu	Leu	Asp	Leu
	210					215					220				
Lys	Pro	Asp	Glu	Leu	Asn	Ala	Leu	Arg	Gly	His	Glu	Ile	Ala	Met	Ile
225					230					235				240	
Tyr	Gln	Asp	Ala	Leu	Ser	Ser	Leu	Asn	Pro	Ser	Met	Leu	Ile	Ser	Ala
			245						250					255	
Gln	Met	Lys	Gln	Leu	Thr	Arg	Arg	Gly	Gly	Lys	Arg	Ser	Ala	Glu	Glu
			260					265					270		
Leu	Leu	Glu	Leu	Val	Gly	Leu	Asp	Pro	Lys	Arg	Thr	Leu	Gln	Ser	Tyr
		275					280					285			
Pro	His	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Val	Leu	Ile	Ala	Met
	290					295					300				
Ala	Leu	Thr	Arg	Asn	Pro	Arg	Leu	Leu	Ile	Ala	Asp	Glu	Pro	Thr	Thr
305					310					315					320

Pro Ala Thr Ser Leu Asn Pro Arg Met Thr Val Arg Glu Gln Leu Leu
55 60 65

gat cca ctt cga gta cac aaa gtt ggc gat gaa gca tcc cgc aac cag 355
Asp Pro Leu Arg Val His Lys Val Gly Asp Glu Ala Ser Arg Asn Gln
70 75 80 85

tgg gtt tca gag ctg atc tcc atg gtt ggc ctc ccg caa tcc gcg ttg 403
Trp Val Ser Glu Leu Ile Ser Met Val Gly Leu Pro Gln Ser Ala Leu
90 95 100

gaa gta ctc ccc cga cag gtt tcc ggt ggc caa cgc caa cgc gtg gcc 451
Glu Val Leu Pro Arg Gln Val Ser Gly Gly Gln Arg Gln Arg Val Ala
105 110 115

att gct cga gca ctt gcg ctg aaa cct gac atc atc gtt gcc gac gaa 499
Ile Ala Arg Ala Leu Ala Leu Lys Pro Asp Ile Ile Val Ala Asp Glu
120 125 130

cca acc tcc gcg ctg gat gta tcc gtt cgt gcg cag gtc ctc aac ctt 547
Pro Thr Ser Ala Leu Asp Val Ser Val Arg Ala Gln Val Leu Asn Leu
135 140 145

ctg ctg gat ctg aaa act gaa ctc ggc ctg gga ttg gta ttc atc tcc 595
Leu Leu Asp Leu Lys Thr Glu Leu Gly Leu Gly Leu Val Phe Ile Ser
150 155 160 165

cac gac atc aac act gtt cgc tac gtt tct gat cgc atc gca gtc atg 643
His Asp Ile Asn Thr Val Arg Tyr Val Ser Asp Arg Ile Ala Val Met
170 175 180

ctg gct gga gaa atc att gag gaa aac acc acc tca gag atc ttc aac 691
Leu Ala Gly Glu Ile Ile Glu Glu Asn Thr Thr Ser Glu Ile Phe Asn
185 190 195

aat gcg cag cag gac tac acc cgc act ctg ctc gaa gcg aca cca tcg 739
Asn Ala Gln Gln Asp Tyr Thr Arg Thr Leu Leu Glu Ala Thr Pro Ser
200 205 210

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<210> 286
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<212> PRT
<213> Corynebacterium glutamicum

<400> 286
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Met Lys Pro Arg Gly Ala Gln Arg Lys Glu Leu Gly Ser Ser Val Ser
35 40 45

Val Val Phe Gln Asp Pro Ala Thr Ser Leu Asn Pro Arg Met Thr Val
50 55 60

Arg Glu Gln Leu Leu Asp Pro Leu Arg Val His Lys Val Gly Asp Glu
 65 70 75 80
 Ala Ser Arg Asn Gln Trp Val Ser Glu Leu Ile Ser Met Val Gly Leu
 85 90 95
 Pro Gln Ser Ala Leu Glu Val Leu Pro Arg Gln Val Ser Gly Gly Gln
 100 105 110
 Arg Gln Arg Val Ala Ile Ala Arg Ala Leu Ala Leu Lys Pro Asp Ile
 115 120 125
 Ile Val Ala Asp Glu Pro Thr Ser Ala Leu Asp Val Ser Val Arg Ala
 130 135 140
 Gln Val Leu Asn Leu Leu Leu Asp Leu Lys Thr Glu Leu Gly Leu Gly
 145 150 155 160
 Leu Val Phe Ile Ser His Asp Ile Asn Thr Val Arg Tyr Val Ser Asp
 165 170 175
 Arg Ile Ala Val Met Leu Ala Gly Glu Ile Ile Glu Glu Asn Thr Thr
 180 185 190
 Ser Glu Ile Phe Asn Asn Ala Gln Gln Asp Tyr Thr Arg Thr Leu Leu
 195 200 205
 Glu Ala Thr Pro Ser Leu Leu Asn Lys Thr Arg Leu
 210 215 220

<210> 287
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1132)
 <223> RXA00760

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 Met Pro Asn Asn Glu
 1 5

ttc cac aca aac cac tcg ttg ggc caa gat gat caa acc cca gat cag 163
 Phe His Thr Asn His Ser Leu Gly Gln Asp Asp Gln Thr Pro Asp Gln
 10 15 20

gct cat ttc ttc cca caa gga cga ggc gag gct cta gtt cga cca ggt 211
 Ala His Phe Phe Pro Gln Gly Arg Gly Glu Ala Leu Val Arg Pro Gly
 25 30 35

caa gag cac ttc atc gca gcc act gat gaa acc gga ctt ggt gcc gtc 259
 Gln Glu His Phe Ile Ala Ala Thr Asp Glu Thr Gly Leu Gly Ala Val
 40 45 50

gat gct gtt gct gat gac tct gca cca acc tcc atg tgg ggc gaa gcg 307
Asp Ala Val Ala Asp Asp Ser Ala Pro Thr Ser Met Trp Gly Glu Ala
55 60 65

tgg cga gac ctt cgt cgt cga cca ctg ttc tgg gtc tct gcg gtg ttg 355
Trp Arg Asp Leu Arg Arg Arg Pro Leu Phe Trp Val Ser Ala Val Leu
70 75 80 85

att att ttg gcg ctt ctc ctg gcc gca gtt ccg cag ctg ttt acc tca 403
Ile Ile Leu Ala Leu Leu Leu Ala Ala Val Pro Gln Leu Phe Thr Ser
90 95 100

acg gat ccc cag ttc tgt gtg ctg gca aac tct ctt gat ggt cca cag 451
Thr Asp Pro Gln Phe Cys Val Leu Ala Asn Ser Leu Asp Gly Pro Gln
105 110 115

tct gga cat ccc ttc gga ttc gac cgt caa ggt tgc gat att ttt gct 499
Ser Gly His Pro Phe Gly Phe Asp Arg Gln Gly Cys Asp Ile Phe Ala
120 125 130

cgt acc gtc tac ggt gct cgt gcc tcg gtc gcc gtc ggt gtg ttg acc 547
Arg Thr Val Tyr Gly Ala Arg Ala Ser Val Ala Val Gly Val Leu Thr
135 140 145

acg tta ctg gtc gcc ctc atc ggt act gta ttt ggt gct ttg gct ggc 595
Thr Leu Leu Val Ala Leu Ile Gly Thr Val Phe Gly Ala Leu Ala Gly
150 155 160 165

ttc ttt ggt ggc atc atg gat acc atc ctc tcc cgc atc acc gac atg 643
Phe Phe Gly Gly Ile Met Asp Thr Ile Leu Ser Arg Ile Thr Asp Met
170 175 180

ttc ttc gcc att cca ctg gtt ctg gca gcc atc gtt gtg atg cag atg 691
Phe Phe Ala Ile Pro Leu Val Leu Ala Ala Ile Val Val Met Gln Met
185 190 195

ttc aag gaa cac cgc acc atc gtc acc gtg gtt ttg gtg ctt ggg ctt 739
Phe Lys Glu His Arg Thr Ile Val Thr Val Val Leu Val Leu Gly Leu
200 205 210

ttc ggc tgg acc aac att gcg cgt att acc cgt gga gcg gtg atg acc 787
Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg Gly Ala Val Met Thr
215 220 225

gca aag aat gaa gag tat gtc acc tcc gca cgt gcg ctt ggt gca tca 835
Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg Ala Leu Gly Ala Ser
230 235 240 245

aaa gcc aag ata ctg ctg tct cac atc atg cca aac gcc gca gca ccc 883
Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro Asn Ala Ala Ala Pro
250 255 260

atc att gtg tat gca act gtg gca ctg gga aca ttc atc gtg gca gag 931
Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr Phe Ile Val Ala Glu
265 270 275

gcg acg ctc tcc ttc ctg ggc att ggc ctt cca cca tca att gtc tcc 979
Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro Pro Ser Ile Val Ser
280 285 290

tgg ggt gct gat atc gcg aag gca caa acc tcc ctt cgt acc caa ccc 1027

Leu Val Leu Gly Leu Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg
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 Gly Ala Val Met Thr Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg
 225 230 235 240
 Ala Leu Gly Ala Ser Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro
 245 250 255
 Asn Ala Ala Ala Pro Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr
 260 265 270
 Phe Ile Val Ala Glu Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro
 275 280 285
 Pro Ser Ile Val Ser Trp Gly Ala Asp Ile Ala Lys Ala Gln Thr Ser
 290 295 300
 Leu Arg Thr Gln Pro Met Val Leu Phe Tyr Pro Ala Met Ala Leu Ala
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 Leu Thr Val Leu Ser Phe Ile Met Met Gly Asp Val Val Arg Asp Ala
 325 330 335
 Leu Asp Pro Lys Ser Arg Lys Arg
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<210> 289
 <211> 1632
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1609)
 <223> RXA02035

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 Met Lys Ile Thr Arg
 1 5
 gga ctc ctg cca tca ttg ctg ttg gca agc aca atc gtg gtg tgg tca 163
 Gly Leu Leu Pro Ser Leu Leu Leu Ala Ser Thr Ile Val Val Ser Ser
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 Cys Ser Ala Gly Ser Thr Ala Tyr Gln Gln Pro Pro Ala Val Asp Gln
 25 30 35
 tca tcc att gtc att gct acc acg gct gct gcg gcg tca ctt gat ttc 259
 Ser Ser Ile Val Ile Ala Thr Thr Ala Ala Ala Ala Ser Leu Asp Phe
 40 45 50
 acc aat gct gcg ggc gct gct att ccg cag gcg atg atg tcc aat att 307
 Thr Asn Ala Ala Gly Ala Ala Ile Pro Gln Ala Met Met Ser Asn Ile
 55 60 65

BGI-131CP

tac gag ggg ctt gtg cgc atc gat gcg gag ggt gag att cag ccg ctg 355
 Tyr Glu Gly Leu Val Arg Ile Asp Ala Glu Gly Glu Ile Gln Pro Leu
 70 75 80 85

ctt gcc acg tcg tgg gat att tca gac gat cgc acc gag tac att ttc 403
 Leu Ala Thr Ser Trp Asp Ile Ser Asp Asp Arg Thr Glu Tyr Ile Phe
 90 95 100

cat ttg cgg gag ggt gtg ctg ttt tcc aac ggc gat ccc ttc aat gct 451
 His Leu Arg Glu Gly Val Leu Phe Ser Asn Gly Asp Pro Phe Asn Ala
 105 110 115

gat tct gcg aag ttt tcc att gat cgg gta aaa act gac tgg acc aat 499
 Asp Ser Ala Lys Phe Ser Ile Asp Arg Val Lys Thr Asp Trp Thr Asn
 120 125 130

ggt ttg aaa agt ggc atg gat gtg gtg gag tcc acc gag gtg att gac 547
 Gly Leu Lys Ser Gly Met Asp Val Val Glu Ser Thr Glu Val Ile Asp
 135 140 145

gat cac acg ctg aaa gtt tcg ctg gtc agg ccg tcc aac caa tgg ttg 595
 Asp His Thr Leu Lys Val Ser Leu Val Arg Pro Ser Asn Gln Trp Leu
 150 155 160 165

tgg agc atg ggt acc gcg atc ggt gcc atg atg acg gag ggg ggc gtc 643
 Trp Ser Met Gly Thr Ala Ile Gly Ala Met Met Thr Glu Gly Gly Val
 170 175 180

gat aag ctg gca act gat ccc gtt ggc acc ggc ccg tac acg gtg acg 691
 Asp Lys Leu Ala Thr Asp Pro Val Gly Thr Gly Pro Tyr Thr Val Thr
 185 190 195

cac tgg gcg ccg ggc cgc gca att ggg ttc ggc gcg ccg gcc gat tat 739
 His Trp Ala Pro Gly Arg Ala Ile Gly Phe Gly Ala Arg Ala Asp Tyr
 200 205 210

tgg ggg cag aag ccg ctt aac gac gcc gca acc atc cgc tac ttc agc 787
 Trp Gly Gln Lys Pro Leu Asn Asp Ala Ala Thr Ile Arg Tyr Phe Ser
 215 220 225

gat gcg acg gcc tcg acc aat gcg ctg caa agc ggt gac gtg gac gtg 835
 Asp Ala Thr Ala Ser Thr Asn Ala Leu Gln Ser Gly Asp Val Asp Val
 230 235 240 245

att tgg gcg atg caa gcg ccc gaa cag ctg gct acg ctg cag gaa tac 883
 Ile Trp Ala Met Gln Ala Pro Glu Gln Leu Ala Thr Leu Gln Glu Tyr
 250 255 260

acc gtg gaa gtg ggc aca acc aat ggt gag atg ttg ctg tcg atg aat 931
 Thr Val Glu Val Gly Thr Thr Asn Gly Glu Met Leu Leu Ser Met Asn
 265 270 275

aat cag cgt gca cct ttt gat gat gtg cgt gtg cgc cag gcg gtg atg 979
 Asn Gln Arg Ala Pro Phe Asp Asp Val Arg Val Arg Gln Ala Val Met
 280 285 290

ttt gcg att gat cgc caa gcc gtc att gat acc gcg ttg gaa ggt tac 1027
 Phe Ala Ile Asp Arg Gln Ala Val Ile Asp Thr Ala Leu Glu Gly Tyr
 295 300 305

ggc acc gac act ggt ggc gtg cct gtt ccg ccg act gat ccg tgg tac 1075

Gly Thr Asp Thr Gly Gly Val Pro Val Pro Pro Thr Asp Pro Trp Tyr
 310 315 320 325
 gag aaa tcc acg atg tac ccc tac gat ccg gac cgc gca cgg gca ttg 1123
 Glu Lys Ser Thr Met Tyr Pro Tyr Asp Pro Asp Arg Ala Arg Ala Leu
 330 335 340
 tta gag gag gcc ggc gcc gag gga acg cgg atc acc atg tcc att cct 1171
 Leu Glu Glu Ala Gly Ala Glu Gly Thr Arg Ile Thr Met Ser Ile Pro
 345 350 355
 tcg ttg ccg tac gct cag gca gcc tct gaa atc ctg tac tcg caa ctg 1219
 Ser Leu Pro Tyr Ala Gln Ala Ala Ser Glu Ile Leu Tyr Ser Gln Leu
 360 365 370
 cga gat gtt ggt ttt gat cct gtg att gaa tca acc gag ttc cca gcc 1267
 Arg Asp Val Gly Phe Asp Pro Val Ile Glu Ser Thr Glu Phe Pro Ala
 375 380 385
 gtc tgg ttg gca cag gtc atg ggg caa aaa gac tac gac atg tca cta 1315
 Val Trp Leu Ala Gln Val Met Gly Gln Lys Asp Tyr Asp Met Ser Leu
 390 395 400 405
 atc gcg cat gtg gaa ccc cgc gac atc ccc acg ctg ttt agc ccc aac 1363
 Ile Ala His Val Glu Pro Arg Asp Ile Pro Thr Leu Phe Ser Pro Asn
 410 415 420
 tac tat ttg ggc ttt gac gac acc gaa acc caa gcc ctc ctc gca gag 1411
 Tyr Tyr Leu Gly Phe Asp Asp Thr Glu Thr Gln Ala Leu Leu Ala Glu
 425 430 435
 gca gac agt tca gca aac gaa gtg gaa ttg atg caa caa gct gtc gat 1459
 Ala Asp Ser Ser Ala Asn Glu Val Glu Leu Met Gln Gln Ala Val Asp
 440 445 450
 cga atc atg gaa caa gcc gtc gcc gac aac ctc atg aac gtg gcc aac 1507
 Arg Ile Met Glu Gln Ala Val Ala Asp Asn Leu Met Asn Val Ala Asn
 455 460 465
 atc gtg gtg atg tca cca gag atc acc ggc att gat ccc aac gtg gtg 1555
 Ile Val Val Met Ser Pro Glu Ile Thr Gly Ile Asp Pro Asn Val Val
 470 475 480 485
 tcc ggg gcg ttg gaa ttg tcg ttg att ggt cgg aaa gaa tcc ggg gta 1603
 Ser Gly Ala Leu Glu Leu Ser Leu Ile Gly Arg Lys Glu Ser Gly Val
 490 495 500
 gcg cag tgagtaaaac aatcgcttgg act 1632
 Ala Gln

<210> 290

<211> 503

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Met Lys Ile Thr Arg Gly Leu Leu Pro Ser Leu Leu Leu Ala Ser Thr
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340 345 350

Thr Met Ser Ile Pro Ser Leu Pro Tyr Ala Gln Ala Ala Ser Glu Ile
355 360 365

Leu Tyr Ser Gln Leu Arg Asp Val Gly Phe Asp Pro Val Ile Glu Ser
370 375 380

Thr Glu Phe Pro Ala Val Trp Leu Ala Gln Val Met Gly Gln Lys Asp
385 390 395 400

Tyr Asp Met Ser Leu Ile Ala His Val Glu Pro Arg Asp Ile Pro Thr
405 410 415

Leu Phe Ser Pro Asn Tyr Tyr Leu Gly Phe Asp Asp Thr Glu Thr Gln
420 425 430

Ala Leu Leu Ala Glu Ala Asp Ser Ser Ala Asn Glu Val Glu Leu Met
435 440 445

Gln Gln Ala Val Asp Arg Ile Met Glu Gln Ala Val Ala Asp Asn Leu
450 455 460

Met Asn Val Ala Asn Ile Val Val Met Ser Pro Glu Ile Thr Gly Ile
465 470 475 480

Asp Pro Asn Val Val Ser Gly Ala Leu Glu Leu Ser Leu Ile Gly Arg
485 490 495

Lys Glu Ser Gly Val Ala Gln
500

<210> 291
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXN01002

<400> 291
gactgctgat accgcacagg atgaaatcac tcgttacggc gagatcctga agaagttctc 60

caactaattt cctgttttcc aataactcaag gtgtgcgcat atg aat tct gat gct 115
Met Asn Ser Asp Ala
1 5

tcg gct acc acc aac tcc tgg gct atc aac ttc gac cat gtg tcg gtg 163
Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe Asp His Val Ser Val
10 15 20

acg tat ccc aat ggg acg aaa gcc ctc gat gat gtt tcc ctc acc atc 211
Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp Val Ser Leu Thr Ile
25 30 35

aat ccc ggt gag atg gtt gcc atc gtg ggt ctg tca gga tcg ggt aaa 259
Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu Ser Gly Ser Gly Lys
40 45 50

tcc acg ctg att cgc acg atc aac ggt ctt gtc cgc gct acg gaa ggc 307
 Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val Arg Ala Thr Glu Gly
 55 60 65

acc gtg acg gtg ggg ccg cat cag atc aac acc ttg aag ggg aaa gca 355
 Thr Val Thr Val Gly Pro His Gln Ile Asn Thr Leu Lys Gly Lys Ala
 70 75 80 85

ctg cgt gat gcc cgt ggg cag atc ggc atg att ttc cag ggg ttc aac 403
 Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile Phe Gln Gly Phe Asn
 90 95 100

ctg tcg gaa cgc agc agt gtg ttc cag aat gtt ttg gtg ggc cgc ttc 451
 Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val Leu Val Gly Arg Phe
 105 110 115

gcg cac aca gcg tgg tgg cgt aac ctc ctc ggg ttt ccc acg gag cac 499
 Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly Phe Pro Thr Glu His
 120 125 130

gac aag cag att gct ttt cac gcg ttg gag tcc gtg ggc att ttg cac 547
 Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val Gly Ile Leu His
 135 140 145

aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga cag aaa cag cgc 595
 Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly Gln Lys Gln Arg
 150 155 160 165

gtt gct att gcg cgc gcc tta tcg caa gat ccg tct gtc atg ctg gca 643
 Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser Val Met Leu Ala
 170 175 180

gat gag cct gtg gca agc ctt gat ccg cca acc gcg cat tcc gtg atg 691
 Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala His Ser Val Met
 185 190 195

cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc acc gtg ttg gtg 739
 Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu Thr Val Leu Val
 200 205 210

aac ttg cac ttg att gat ttg gct cgt caa tac acc aca agg ctt gtg 787
 Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr Thr Arg Leu Val
 215 220 225

ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct atc tct gag gcc 835
 Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro Ile Ser Glu Ala
 230 235 240 245

acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc atc cag gct aaa 883
 Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro Ile Gln Ala Lys
 250 255 260

gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca ctt 927
 Asp Leu Leu Gly Asp Arg Ala
 265

<210> 292

<211> 268

<212> PRT

Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala
50 55 60

His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu
 65 70 75 80

Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr
 85 90 95

Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro
 100 105 110

Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro
 115 120 125

Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
 130 135

<210> 295
 <211> 969
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(946)
 <223> RXN01000

<400> 295
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tcattgaagt aatctccaac gcacttcgaa agaggctggt atg agc acc tta acc 115
 Met Ser Thr Leu Thr
 1 5

tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac 163
 Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn
 10 15 20

aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt 211
 Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu
 25 30 35

ata gct acc ggc acg ctc aag atc gag tgg aat gag ctt ccg cag atg 259
 Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met
 40 45 50

ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat 307
 Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp
 55 60 65

tgg tcg aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc 355
 Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala
 70 75 80 85

atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg 403
 Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu
 90 95 100

gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt 451
 Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val
 105 110 115

000000-12000000

tta cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc 499
 Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile
 120 125 130

gca att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg 547
 Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala
 135 140 145

ctc gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat 595
 Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr
 150 155 160 165

gaa gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca 643
 Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala
 170 175 180

gcg ggt gga act acg ccg gag gtt ctg ccg tgg gcg ttg tgg cca cag 691
 Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln
 185 190 195

gtt gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac 739
 Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn
 200 205 210

atc cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt 787
 Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly
 215 220 225

agt atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc 835
 Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly
 230 235 240 245

atg ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc 883
 Met Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile
 250 255 260

tcc ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc 931
 Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val
 265 270 275

gtg gca cca agc aac tgacgctcca ccaagcatcc gca 969
 Val Ala Pro Ser Asn
 280

<210> 296

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Met Ser Thr Leu Thr Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro
1 5 10 15

Pro Ala Arg Pro Asn Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala
20 25 30

Ala Leu Ile Val Leu Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn
35 40 45

Glu Leu Pro Gln Met Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met
 50 55 60
 Phe Ser Asp Pro Asp Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met
 65 70 75 80
 Trp Arg Ser Ile Ala Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val
 85 90 95
 Val Ser Val Pro Leu Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr
 100 105 110
 Trp Leu Arg Thr Val Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe
 115 120 125
 Pro Glu Val Val Ile Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr
 130 135 140
 Pro Phe Thr Gly Ala Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln
 145 150 155 160
 Ala Lys Trp Thr Tyr Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser
 165 170 175
 Glu Ala Val Arg Ala Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp
 180 185 190
 Ala Leu Trp Pro Gln Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr
 195 200 205
 Arg Phe Glu Ile Asn Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly
 210 215 220
 Ala Gly Gly Ile Gly Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln
 225 230 235 240
 Trp Asp Thr Val Gly Met Leu Leu Ile Val Val Val Val Ala Thr Met
 245 250 255
 Ile Val Asp Leu Ile Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly
 260 265 270
 Ala Ser Asp Arg Val Val Ala Pro Ser Asn
 275 280

<210> 297

<211> 563

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(540)

<223> FRXA01000

<400> 297

atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt tta 48
 Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val Leu
 1 5 10 15

cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc gca 96
 Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile Ala
 20 25 30

att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg ctc 144
 Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu
 35 40 45

gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat gaa 192
 Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu
 50 55 60

gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca gcg 240
 Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala Ala
 65 70 75 80

ggt gga act acg ccg gag gtt ctg ccg tgg gcg ttg tgg cca cag gtt 288
 Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln Val
 85 90 95

gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac atc 336
 Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn Ile
 100 105 110

cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt agt 384
 Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Ser
 115 120 125

atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc atg 432
 Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly Met
 130 135 140

ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc tcc 480
 Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile Ser
 145 150 155 160

ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc gtg 528
 Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val Val
 165 170 175

gca cca agc aac tgacgctcca ccaagcatcc gca 563
 Ala Pro Ser Asn
 180

<210> 298

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val Leu
 1 5 10 15

Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile Ala
 20 25 30

Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu
 35 40 45

Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu

Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr Leu Gln Met Ala Leu
 70 75 80 85
 gtt gga gct gtc ttg tct gct gcc gta tcg gtg cct ttg acg ttg tgg 403
 Val Gly Ala Val Leu Ser Ala Ala Val Ser Val Pro Leu Thr Leu Trp
 90 95 100
 gca gcg cag gca acc aac acc agt gcg att ggt cgt ggc att gtc cgc 451
 Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly Arg Gly Ile Val Arg
 105 110 115
 acc atc att aac gtg gtg cgc tct gtc ccc gac ttg gtg tat gcc acc 499
 Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp Leu Val Tyr Ala Thr
 120 125 130
 atc ttg gtc gcc atg gtt ggt gtc ggc gca tta cct ggc att ttg acg 547
 Ile Leu Val Ala Met Val Gly Val Gly Ala Leu Pro Gly Ile Leu Thr
 135 140 145
 ctg ttt ctg ttc aac ctg ggc atc gtg gtc aag ctt gtc tct gag gcc 595
 Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys Leu Val Ser Glu Ala
 150 155 160 165
 att gat tcc act gag cat ccc tat atg gaa gca gga cgc gca gca ggt 643
 Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala Gly Arg Ala Ala Gly
 170 175 180
 gga tca cag ttc caa atc aac cga gtc tcc gcg ctt cct gaa gtc atg 691
 Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala Leu Pro Glu Val Met
 185 190 195
 ccg ctc ttt gcc aac caa tgg ctc tac acc cta gag ctg aat gta cgc 739
 Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu Glu Leu Asn Val Arg
 200 205 210
 atc tcc gcc atc ctt ggc atc gtg ggc gca ggt ggc atc ggc agg ctg 787
 Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Arg Leu
 215 220 225
 ctt gat gaa cgc cga gct ttc tat gcc tac gcg gat gtt tcc gtg atc 835
 Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala Asp Val Ser Val Ile
 230 235 240 245
 att ctg gaa atc ctc atc gtg gtg att gtc att gaa gta atc tcc aac 883
 Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile Glu Val Ile Ser Asn
 250 255 260
 gca ctt cga aag agg ctg gta tgagcacctt aacctctcac cgc 927
 Ala Leu Arg Lys Arg Leu Val
 265

<210> 300

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met Thr Thr Pro Ser Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly
 1 5 10 15

Val Lys Thr Tyr Leu Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala
 20 25 30
 Thr Ala Thr Pro Ala Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile
 35 40 45
 Ala Ala Asn Trp Arg Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln
 50 55 60
 Pro Asn Phe Ala Phe Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr
 65 70 75 80
 Leu Gln Met Ala Leu Val Gly Ala Val Leu Ser Ala Ala Val Ser Val
 85 90 95
 Pro Leu Thr Leu Trp Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly
 100 105 110
 Arg Gly Ile Val Arg Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp
 115 120 125
 Leu Val Tyr Ala Thr Ile Leu Val Ala Met Val Gly Val Gly Ala Leu
 130 135 140
 Pro Gly Ile Leu Thr Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys
 145 150 155 160
 Leu Val Ser Glu Ala Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala
 165 170 175
 Gly Arg Ala Ala Gly Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala
 180 185 190
 Leu Pro Glu Val Met Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu
 195 200 205
 Glu Leu Asn Val Arg Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly
 210 215 220
 Gly Ile Gly Arg Leu Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala
 225 230 235 240
 Asp Val Ser Val Ile Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile
 245 250 255
 Glu Val Ile Ser Asn Ala Leu Arg Lys Arg Leu Val
 260 265

<210> 301

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(594)

<223> RXN00193

<400> 301

aaa gct ttc tnc caa cgc gaa ggt ttc atc tca gcc ttc ggt ttc acc 48

Lys Ala Phe Xaa Gln Arg Glu Gly Phe Ile Ser Ala Phe Gly Phe Thr
 1 5 10 15
 gtc ctc gtg gtc atc gtc tcc gtg atc aca gtc aac atc ttc gcc ttc 96
 Val Leu Val Val Ile Val Ser Val Ile Thr Val Asn Ile Phe Ala Phe
 20 25 30
 ctc ttg gcg tgg ttg ctg acc cgc aaa ctc cgc ggt acc aac ttt ttc 144
 Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe
 35 40 45
 cgc aca gtc ttc ttt atg ccg aac ctt atc ggc ggc att gtg ctg ggt 192
 Arg Thr Val Phe Phe Met Pro Asn Leu Ile Gly Gly Ile Val Leu Gly
 50 55 60
 tat acc tgg cag acc atg atc aac gcc gtg ctt tcg cac tat gcc acg 240
 Tyr Thr Trp Gln Thr Met Ile Asn Ala Val Leu Ser His Tyr Ala Thr
 65 70 75 80
 act att agc gcg gac tgg aaa ttc ggc tac gcc ggc ctc atc atg cta 288
 Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu
 85 90 95
 ctt aac tgg cag ctc atc ggc tac atg atg atc att tac atc gcc ggc 336
 Leu Asn Trp Gln Leu Ile Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly
 100 105 110
 ctg caa aac gtc cca cca gag ctc att gag gct gcc gaa ctc gac ggc 384
 Leu Gln Asn Val Pro Pro Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly
 115 120 125
 gtc aac aag tgg gag atg ctg cgg cac gtc act att ccg atg gtc atg 432
 Val Asn Lys Trp Glu Met Leu Arg His Val Thr Ile Pro Met Val Met
 130 135 140
 cca tcc atc acc atc tgc ctc ttt ttg act ttg tcg aac tcc ttt aag 480
 Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys
 145 150 155 160
 ctc ttc gac cag aac ctg gcg ctg acc aac ggc gct cct ggc ggg caa 528
 Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln
 165 170 175
 act gag atg gtg gcg ctc aac atc atc aac acg ctg ttt aac cgt atg 576
 Thr Glu Met Val Ala Leu Asn Ile Ile Asn Thr Leu Phe Asn Arg Met
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      Met Gln Ala Thr Leu Lys Lys Tyr Phe Pro Val Phe
      1             5             10
gtc ttg ccc acc ctt ctg gca ttc atg att gcc ttc ttg gtg ccg ttc 158
Val Leu Pro Thr Leu Leu Ala Phe Met Ile Ala Phe Leu Val Pro Phe
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atc gtg ggt ttc ttc ctc tcc ttt acg aag ttc acc act atc acc aac 206
Ile Val Gly Phe Phe Leu Ser Phe Thr Lys Phe Thr Thr Ile Thr Asn
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Glu Gly Phe Ile Ser Ala Phe Gly Phe Thr Val Leu Val Val Ile Val	
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Ser Val Ile Thr Val Asn Ile Phe Ala Phe Leu Leu Ala Trp Leu Leu	
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Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe Arg Thr Val Phe Phe Met	
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ccg aac ctt atc ggc ggc att gtg ctg ggt tat acc tgg cag acc atg	446
Pro Asn Leu Ile Gly Gly Ile Val Leu Gly Tyr Thr Trp Gln Thr Met	
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Ile Asn Ala Val Leu Ser His Tyr Ala Thr Thr Ile Ser Ala Asp Trp	
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Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu Leu Asn Trp Gln Leu Ile	
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Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly Leu Gln Asn Val Pro Pro	
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gag ctc att gag gct gcc gaa ctc gac ggc gtc aac aag tgg gag atg	638
Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly Val Asn Lys Trp Glu Met	
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Leu Arg His Val Thr Ile Pro Met Val Met Pro Ser Ile Thr Ile Cys	
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Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys Leu Phe Asp Gln Asn Leu	
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225 230 235	
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Asn Ile Ile Asn Thr Leu Phe Asn Arg Met Asn Val Glu Gly Val Gly	
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Gln Ala Lys Ala Val Ile Phe Val Val Val Val Val Val Ile Ala Tyr	
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Phe	Leu	Ser	Phe	Thr	Lys	Phe	Thr	Thr	Ile	Thr	Asn	Ala	Lys	Trp	Val
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Gly	Ile	Asp	Asn	Tyr	Val	Lys	Ala	Phe	Ser	Gln	Arg	Glu	Gly	Phe	Ile
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Ser	Ala	Phe	Gly	Phe	Thr	Val	Leu	Val	Val	Ile	Val	Ser	Val	Ile	Thr
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Val	Asn	Ile	Phe	Ala	Phe	Leu	Leu	Ala	Trp	Leu	Leu	Thr	Arg	Lys	Leu
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Arg	Gly	Thr	Asn	Phe	Phe	Arg	Thr	Val	Phe	Phe	Met	Pro	Asn	Leu	Ile
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Gly	Gly	Ile	Val	Leu	Gly	Tyr	Thr	Trp	Gln	Thr	Met	Ile	Asn	Ala	Val
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Leu	Ser	His	Tyr	Ala	Thr	Thr	Ile	Ser	Ala	Asp	Trp	Lys	Phe	Gly	Tyr
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Ala	Gly	Leu	Ile	Met	Leu	Leu	Asn	Trp	Gln	Leu	Ile	Gly	Tyr	Met	Met
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Ile	Ile	Tyr	Ile	Ala	Gly	Leu	Gln	Asn	Val	Pro	Pro	Glu	Leu	Ile	Glu
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Ala	Ala	Glu	Leu	Asp	Gly	Val	Asn	Lys	Trp	Glu	Met	Leu	Arg	His	Val
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Thr	Ile	Pro	Met	Val	Met	Pro	Ser	Ile	Thr	Ile	Cys	Leu	Phe	Leu	Thr
		195					200					205			

Leu	Ser	Asn	Ser	Phe	Lys	Leu	Phe	Asp	Gln	Asn	Leu	Ala	Leu	Thr	Asn
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Gly	Ala	Pro	Gly	Gly	Gln	Thr	Glu	Met	Val	Ala	Leu	Asn	Ile	Ile	Asn
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Thr	Leu	Phe	Asn	Arg	Met	Asn	Val	Glu	Gly	Val	Gly	Gln	Ala	Lys	Ala
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Val	Ile	Phe	Val	Val	Val	Val	Val	Val	Ile	Ala	Tyr	Phe	Gln	Leu	Arg
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Ala	Thr	Arg	Ser	Lys	Glu	Ile	Glu	Ala
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Val Ser Thr Leu Ile 5																
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Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg Ala Lys Arg Ser Arg 20																
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Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu Ala Pro Asn Leu Leu 35																
25 30																
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Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu Asp Asn Phe Arg Leu 50																
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Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser Asp Thr Leu Gln Val 85																
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Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala Val Ile Gly Ser Met 100																
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Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro Phe Val Ile Ser Gly 130																
120 125																
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Ala Ala Ile Gly Val Ala Phe Gln Phe Val Phe Asp Pro Asn Phe Gly 145																
135 140																
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Leu Val Gln Asp Leu Leu Gly Arg Ile Gly Val Asp Ser Pro Gln Phe 165																
150 155 160																
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Asp Thr Leu Gln Val Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala
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 Val Ile Gly Ser Met Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp
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 Asp Pro Asn Phe Gly Leu Val Gln Asp Leu Leu Gly Arg Ile Gly Val
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 Asp Ser Pro Gln Phe Tyr Gln Asn Pro Asn Trp Ala Leu Phe Met Val
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 Thr Phe Thr Phe Val Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr
 180 185 190
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 195 200 205
 Val Asp Gly Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro
 210 215 220
 Gln Leu Arg Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn
 225 230 235 240
 Ser Val Gln Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro
 245 250 255
 Leu Gly Asn Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr
 260 265 270
 Phe Thr Asn Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu
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gcg agc gcg tgg aca cgt ttt tgg aag gtt act ctt ccg cag ctt cgc 144
 Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg
 35 40 45

cca acc acg ttc ttc ctt tct att act gtc acg ctg aac tcg gtt cag 192
 Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln
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 Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn
 65 70 75 80

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 Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn
 85 90 95

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 Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu
 100 105 110

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 Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln
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 Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn
 65 70 75 80
 Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn
 85 90 95
 Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu
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120

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Val Ser Thr Leu Ile
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Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg Ala Lys Arg Ser Arg
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Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu Ala Pro Asn Leu Leu
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Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu Asp Asn Phe Arg Leu
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Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser Asp Thr Leu Gln Val
70 75 80 85

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Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp Gln Lys Leu Phe Gly
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cgt aac ttt gtg cgt tcc atg gtg ttt gcc ccg ttt gtg att tcc ggt 499
Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro Phe Val Ile Ser Gly
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135 140 145

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 Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val
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 Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala
 70 75 80 85
 cgc gct ggt ctc ttc ctg gcc atg cag tat cca act gaa atc cct ggc 403
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 Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly
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 gag gct cct aag ctt cgc gag tgg gtt aag gaa gtc cgc acc gct cag 499
 Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu Val Arg Thr Ala Gln
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 gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa 547
 Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu
 135 140 145
 ggt ttc tcc ggt ggc gag aag aag cgc cac gag gtt ctg cag ctt gat 595
 Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu Val Leu Gln Leu Asp
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 170 175 180
 gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag 691
 Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys
 185 190 195
 cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc 739
 Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile
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 Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val Phe Ala Asn Gly Gln
 215 220 225
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Ala Thr Ala Leu Tyr Ala Trp Asn Gly Trp Glu Ala Val Ala Gly Phe
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ccc atc ggt ggt ctg gtg atg gga cat gtt gcc gat aag atc agt cgc 403
 Pro Ile Gly Gly Leu Val Met Gly His Val Gly Asp Lys Ile Ser Arg
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Met Ser Thr Leu Glu
1 5

atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163
Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu
10 15 20

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Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr Ile Asn Ser Gly Glu
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Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala
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tac acc ctt ggt gga cac cca cgc tac gag gta acc gca ggc gag gtc 307
Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val
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170 175 180

gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag 691
Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys
185 190 195

cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc 739
Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile
200 205 210

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215 220 225

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 35 40 45

Lys Ser Thr Leu Ala Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val
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 65 70 75 80

Val Asp Glu Arg Ala Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro
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 130 135 140

Arg Ser Val Asn Glu Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu
 145 150 155 160

Val Leu Gln Leu Asp Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu
 165 170 175

Thr Asp Ser Gly Leu Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly
 180 185 190

Ile Asn Ser Tyr Lys Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr
 195 200 205

His Tyr Lys Arg Ile Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val
 210 215 220

Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp
 225 230 235 240

Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys
245 250

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<211> 1461

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<213> Corynebacterium glutamicum

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<222> (101)..(1438)

<223> RXN01995

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Met Asp Ile Arg Gln
1 5

aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt 163
Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe
10 15 20

atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg 211
Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met
25 30 35

tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc 259
Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser
40 45 50

cag ctt ggt gtg ctg ctg agt tcc gcg ctg ttc ggc atg acc gct gga 307
Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly
55 60 65

tct ttg ctg ttc ggt ccg atc ggt gac cgt ttc ggc cgt aag aat gcc 355
Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala
70 75 80 85

ctg atg atc gcg ctg ctg ttc aac gtg gtg gga ttg gta ttg tcc gcc 403
Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly Leu Val Leu Ser Ala
90 95 100

acc gcg cag tcc gca ggc cag ttg ggc gtg tgg cgt ttg atc act ggt 451
Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp Arg Leu Ile Thr Gly
105 110 115

atc ggc atc ggc gga atc ctc gcc tgc atc aca gtg gtg atc agt gag 499
Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr Val Val Ile Ser Glu
120 125 130

ttc tcc aac aac aaa aac cgc ggc atg gcc atg tcc atc tac gct gct 547
Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met Ser Ile Tyr Ala Ala
135 140 145

ggt tac ggc atc ggc gcg tcc ttg ggc ggt ttc ggc gca gcg cag ctc 595
Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe Gly Ala Ala Gln Leu
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114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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 Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala Ala Gly Ala Ile Ala
 170 175 180

act ggt atc gcc acc atc gct act ttc ttc ttc ctg cca gaa tcc gtt 691
 Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe Leu Pro Glu Ser Val
 185 190 195

gat tgg ctg agc act cgc cgc cct gcg ggc gct cgc gac aag atc aat 739
 Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala Arg Asp Lys Ile Asn
 200 205 210

tac att gcg cgc cgc ctg ggc aaa gtc ggt acc ttt gag ctt cca ggc 787
 Tyr Ile Ala Arg Arg Leu Gly Lys Val Gly Thr Phe Glu Leu Pro Gly
 215 220 225

gaa caa agc ttg tcg acg aaa aaa gcc ggt ctc caa tcg tat gca gtg 835
 Glu Gln Ser Leu Ser Thr Lys Lys Ala Gly Leu Gln Ser Tyr Ala Val
 230 235 240 245

ctc gtt aac aaa gag aac cgt gga acc agc atc aag ctg tgg gtt gcg 883
 Leu Val Asn Lys Glu Asn Arg Gly Thr Ser Ile Lys Leu Trp Val Ala
 250 255 260

ttc ggc atc gtg atg ttc ggc ttc tac ttc gcc aac act tgg acc ccg 931
 Phe Gly Ile Val Met Phe Gly Phe Tyr Phe Ala Asn Thr Trp Thr Pro
 265 270 275

aag ctg ctc gtg gaa acc gga atg tca gaa cag cag ggc atc atc ggt 979
 Lys Leu Leu Val Glu Thr Gly Met Ser Glu Gln Gln Gly Ile Ile Gly
 280 285 290

ggt ttg atg ttg tcc atg ggt gga gca ttc ggc tcc ctg ctc tac ggt 1027
 Gly Leu Met Leu Ser Met Gly Gly Ala Phe Gly Ser Leu Leu Tyr Gly
 295 300 305

ttc ctc acc acc aag ttc agc tcc cga aac aca ctg atg acc ttc atg 1075
 Phe Leu Thr Thr Lys Phe Ser Ser Arg Asn Thr Leu Met Thr Phe Met
 310 315 320 325

gtg ctg tcc gcc ctg acg ctg atc ctg ttc att tcc tcc acc tct gtt 1123
 Val Leu Ser Gly Leu Thr Leu Ile Leu Phe Ile Ser Ser Thr Ser Val
 330 335 340

cca tcc atc gcg ttt gcc agc ggc gtt gtc gtg ggc atg ctg atc aat 1171
 Pro Ser Ile Ala Phe Ala Ser Gly Val Val Val Gly Met Leu Ile Asn
 345 350 355

ggt tgt gtg gct ggt ctg tac acc ctg tcc cca cag ctg tac tcc gct 1219
 Gly Cys Val Ala Gly Leu Tyr Thr Leu Ser Pro Gln Leu Tyr Ser Ala
 360 365 370

gaa gta cgc acc act ggt gtg ggc gct gcg att ggt atg ggt cgt gtc 1267
 Glu Val Arg Thr Thr Gly Val Gly Ala Ala Ile Gly Met Gly Arg Val
 375 380 385

ggt gcg att tcc gcg cca ctg ctg gtg ggt ggc ctg ctg gat tct ggc 1315
 Gly Ala Ile Ser Ala Pro Leu Leu Val Gly Gly Leu Leu Asp Ser Gly
 390 395 400 405

tgc 1461

<213> Corynebacterium glutamicum

Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg Leu Gly Lys Val Gly Thr

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Phe Glu Leu Pro Gly	Glu Gln Ser Leu Ser	Thr Lys Lys Ala Gly Leu
225	230	235 240
Gln Ser Tyr Ala Val	Leu Val Asn Lys Glu	Asn Arg Gly Thr Ser Ile
245	250	255
Lys Leu Trp Val Ala Phe	Gly Ile Val Met Phe	Gly Phe Tyr Phe Ala
260	265	270
Asn Thr Trp Thr Pro Lys	Leu Leu Val Glu Thr	Gly Met Ser Glu Gln
275	280	285
Gln Gly Ile Ile Gly Gly	Leu Met Leu Ser Met	Gly Gly Ala Phe Gly
290	295	300
Ser Leu Leu Tyr Gly Phe	Leu Thr Thr Lys Phe	Ser Ser Arg Asn Thr
305	310	315 320
Leu Met Thr Phe Met Val	Leu Ser Gly Leu Thr	Leu Ile Leu Phe Ile
325	330	335
Ser Ser Thr Ser Val Pro	Ser Ile Ala Phe Ala	Ser Gly Val Val Val
340	345	350
Gly Met Leu Ile Asn Gly	Cys Val Ala Gly Leu	Tyr Thr Leu Ser Pro
355	360	365
Gln Leu Tyr Ser Ala Glu	Val Arg Thr Thr Gly	Val Gly Ala Ala Ile
370	375	380
Gly Met Gly Arg Val Gly	Ala Ile Ser Ala Pro	Leu Leu Val Gly Gly
385	390	395 400
Leu Leu Asp Ser Gly Trp	Ser Pro Thr Gln Leu	Tyr Val Gly Val Ala
405	410	415
Val Ile Val Ile Ala Gly	Ala Thr Ala Leu Ile	Gly Met Arg Thr Gln
420	425	430
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435	440	445

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 <223> FRXA01995

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 Met Asp Ile Arg Gln
 1 5

aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt 163
 Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe
 10 15 20

atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg 211
 Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met
 25 30 35

tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc 259
 Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser
 40 45 50

cag ctt ggt gtg ctg ctg agt tcc gcg ctg ttc ggc atg acc gct gga 307
 Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly
 55 60 65

tct ttg ctg ttc ggt ccg atc ggt gac cgt ttc ggc cgt aag aat gcc 355
 Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala
 70 75 80 85

ctg atg atc gcg ctg ctg ttc aac gtg gtg gga ttg gta ttg tcc gcc 403
 Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly Leu Val Leu Ser Ala
 90 95 100

acc gcg cag tcc gca ggc cag ttg ggc gtg tgg cgt ttg atc act ggt 451
 Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp Arg Leu Ile Thr Gly
 105 110 115

atc ggc atc ggc gga atc ctc gcc tgc atc aca gtg gtg atc agt gag 499
 Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr Val Val Ile Ser Glu
 120 125 130

ttc tcc aac aac aaa aac cgc ggc atg gcc atg tcc atc tac gct gct 547
 Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met Ser Ile Tyr Ala Ala
 135 140 145

ggt tac ggc atc ggc gcg tcc ttg ggc ggt ttc ggc gca gcg cag ctc 595
 Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe Gly Ala Ala Gln Leu
 150 155 160 165

atc cca aca ttt gga tgg cgc tcc gtg ttc gca gcc ggt gcg atc gca 643
 Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala Ala Gly Ala Ile Ala
 170 175 180

act ggt atc gcc acc atc gct act ttc ttc ttc ctg cca gaa tcc gtt 691
 Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe Leu Pro Glu Ser Val
 185 190 195

gat tgg ctg agc act cgc cgc cct gcg ggc gct cgc gac aag atc aat 739
 Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala Arg Asp Lys Ile Asn
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tac att gcg cgc cgc
 Tyr Ile Ala Arg Arg 754
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<211> 218

<212> PRT

<213> Corynebacterium glutamicum

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Asp Val Leu Ala Met Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe
35 40 45

Gly Leu Ser Gly Ser Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe
50 55 60

Gly Met Thr Ala Gly Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe
65 70 75 80

Gly Arg Lys Asn Ala Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly
85 90 95

Leu Val Leu Ser Ala Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp
100 105 110

Arg Leu Ile Thr Gly Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr
115 120 125

Val Val Ile Ser Glu Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met
130 135 140

Ser Ile Tyr Ala Ala Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe
145 150 155 160

Gly Ala Ala Gln Leu Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala
165 170 175

Ala Gly Ala Ile Ala Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe
180 185 190

Leu Pro Glu Ser Val Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala
195 200 205

Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg
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<222> (101)..(1204)

<223> RXA01188

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Met Met Asn Gly Val

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gta	cag	cct	cag	gaa	cat	ctc	gat	gca	acg	ttg	att	gct	gca	gac	ttc	163	
Val	Gln	Pro	Gln	Glu	His	Leu	Asp	Ala	Thr	Leu	Ile	Ala	Ala	Asp	Phe		
				10						15						20	
cac	ggc	aac	ccc	gaa	aac	tct	ggg	gac	cgc	aaa	gag	cgc	ctg	aat	ttt	211	
His	Gly	Asn	Pro	Glu	Asn	Ser	Gly	Asp	Arg	Lys	Glu	Arg	Leu	Asn	Phe		
				25						30						35	
caa	ggg	tgg	aag	tat	gcc	ctt	aat	cgc	acg	gtc	agg	gat	gtt	ttt	cca	259	
Gln	Gly	Trp	Lys	Tyr	Ala	Leu	Asn	Arg	Thr	Val	Arg	Asp	Val	Phe	Pro		
				40						45						50	
gat	ggc	ctg	ctc	gat	ttg	gcg	gcc	ttg	ttg	acg	ttc	ttt	tcc	att	ctg	307	
Asp	Gly	Leu	Leu	Asp	Leu	Ala	Ala	Leu	Leu	Thr	Phe	Phe	Ser	Ile	Leu		
				55						60						65	
tcg	atc	gcc	cct	gca	gtg	ctg	ctg	ggc	tat	tcg	gtg	atc	acg	att	ttt	355	
Ser	Ile	Ala	Pro	Ala	Val	Leu	Leu	Gly	Tyr	Ser	Val	Ile	Thr	Ile	Phe		
				70						75						85	
ctg	gcc	agt	gac	tcc	acc	gaa	atc	ctc	aac	ctt	gtc	cgc	gat	gag	gta	403	
Leu	Ala	Ser	Asp	Ser	Thr	Glu	Ile	Leu	Asn	Leu	Val	Arg	Asp	Glu	Val		
				90						95						100	
aat	cag	tac	gtt	ccg	gaa	gat	caa	tcc	cat	gtt	gtc	aac	ggc	gtg	att	451	
Asn	Gln	Tyr	Val	Pro	Glu	Asp	Gln	Ser	His	Val	Val	Asn	Gly	Val	Ile		
				105						110						115	
gat	tcg	atc	gca	ggc	tcg	gca	gct	gca	ggg	cag	gtc	ggg	gtc	gcg	gtc	499	
Asp	Ser	Ile	Ala	Gly	Ser	Ala	Ala	Ala	Gly	Gln	Val	Gly	Val	Ala	Val		
				120						125						130	
ggg	gtg	atc	acg	gca	ttg	tgg	aca	tct	tcg	gca	tat	gtg	cgc	gct	ttt	547	
Gly	Val	Ile	Thr	Ala	Leu	Trp	Thr	Ser	Ser	Ala	Tyr	Val	Arg	Ala	Phe		
				135						140						145	
tcc	aga	tgt	gcc	aac	gct	gtt	tat	ggc	cga	agc	gaa	ggc	cgc	aca	ttg	595	
Ser	Arg	Cys	Ala	Asn	Ala	Val	Tyr	Gly	Arg	Ser	Glu	Gly	Arg	Thr	Leu		
				150						155						160	
atc	aaa	cgc	tgg	gca	atg	ctg	ctt	ttc	ctc	aac	ctt	gct	ttg	ctg	ctt	643	
Ile	Lys	Arg	Trp	Ala	Met	Leu	Leu	Phe	Leu	Asn	Leu	Ala	Leu	Leu	Leu		
				170						175						180	
gga	atc	atc	atc	att	ttg	gtc	tcc	tgg	gtg	ctc	aac	gag	acc	ttg	gtg	691	
Gly	Ile	Ile	Ile	Ile	Leu	Val	Ser	Trp	Val	Leu	Asn	Glu	Thr	Leu	Val		
				185						190						195	
atg	gga	att	ttc	gcc	ccc	atc	gcg	gaa	cca	ctt	cat	ctc	acg	aat	gtg	739	
Met	Gly	Ile	Phe	Ala	Pro	Ile	Ala	Glu	Pro	Leu	His	Leu	Thr	Asn	Val		
				200						205						210	
ctc	agc	ttc	ctc	acg	gac	cgg	ttc	atg	ccg	atc	tgg	atc	tgg	gtg	cgg	78	

tac tgg gcc ccg aac gcc cgc ccg tgg aag ttt cgc tgg ctc agc ctc 883
 Tyr Trp Ala Pro Asn Ala Arg Pro Trp Lys Phe Arg Trp Leu Ser Leu
 250 255 260

gga tca ttc ttg gcg atc gtt ggc atc ctg ctc gca ggc gtg ggc ttg 931
 Gly Ser Phe Leu Ala Ile Val Gly Ile Leu Leu Ala Gly Val Gly Leu
 265 270 275

aat ttc tac ttc acg ctg ttc gcc gct ttt agt tcc tac ggc gcg gtg 979
 Asn Phe Tyr Phe Thr Leu Phe Ala Ala Phe Ser Ser Tyr Gly Ala Val
 280 285 290

ggt tgc ctg ctc gcg gtt ttt att gcg ctg tgg gtg ttc aac att tgc 1027
 Gly Ser Leu Leu Ala Val Phe Ile Ala Leu Trp Val Phe Asn Ile Cys
 295 300 305

tta atc atc ggc ctg aaa atc gac gtg gag atc agc cgc gcc aag caa 1075
 Leu Ile Ile Gly Leu Lys Ile Asp Val Glu Ile Ser Arg Ala Lys Gln
 310 315 320 325

ctg cag gca gga atg ccg gcg gag gat tac agt tta gtg cca cca cgc 1123
 Leu Gln Ala Gly Met Pro Ala Glu Asp Tyr Ser Leu Val Pro Pro Arg
 330 335 340

tct atc gag aag gtg gcg aaa atg aag cag cgc cag cag cgc ttg atg 1171
 Ser Ile Glu Lys Val Ala Lys Met Lys Gln Arg Gln Gln Arg Leu Met
 345 350 355

gat cag gct gcg gcg atc cgg gag gaa agc aat taaaaaattg cttatcgacg 1224
 Asp Gln Ala Ala Ile Arg Glu Glu Ser Asn
 360 365

tcc 1227

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 <213> Corynebacterium glutamicum

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 20 25 30

Glu Arg Leu Asn Phe Gln Gly Trp Lys Tyr Ala Leu Asn Arg Thr Val
 35 40 45

Arg Asp Val Phe Pro Asp Gly Leu Leu Asp Leu Ala Ala Leu Leu Thr
 50 55 60

Phe Phe Ser Ile Leu Ser Ile Ala Pro Ala Val Leu Leu Gly Tyr Ser
 65 70 75 80

Val Ile Thr Ile Phe Leu Ala Ser Asp Ser Thr Glu Ile Leu Asn Leu
 85 90 95

Val Arg Asp Glu Val Asn Gln Tyr Val Pro Glu Asp Gln Ser His Val

100					105					110					
Val	Asn	Gly	Val	Ile	Asp	Ser	Ile	Ala	Gly	Ser	Ala	Ala	Ala	Gly	Gln
	115						120					125			
Val	Gly	Val	Ala	Val	Gly	Val	Ile	Thr	Ala	Leu	Trp	Thr	Ser	Ser	Ala
	130					135					140				
Tyr	Val	Arg	Ala	Phe	Ser	Arg	Cys	Ala	Asn	Ala	Val	Tyr	Gly	Arg	Ser
145					150					155					160
Glu	Gly	Arg	Thr	Leu	Ile	Lys	Arg	Trp	Ala	Met	Leu	Leu	Phe	Leu	Asn
				165					170					175	
Leu	Ala	Leu	Leu	Leu	Gly	Ile	Ile	Ile	Ile	Leu	Val	Ser	Trp	Val	Leu
		180					185						190		
Asn	Glu	Thr	Leu	Val	Met	Gly	Ile	Phe	Ala	Pro	Ile	Ala	Glu	Pro	Leu
	195						200					205			
His	Leu	Thr	Asn	Val	Leu	Ser	Phe	Leu	Thr	Asp	Arg	Phe	Met	Pro	Ile
	210					215					220				
Trp	Ile	Trp	Val	Arg	Phe	Pro	Val	Ile	Val	Gly	Val	Leu	Ile	Met	Phe
225					230					235					240
Val	Ala	Thr	Leu	Tyr	Tyr	Trp	Ala	Pro	Asn	Ala	Arg	Pro	Trp	Lys	Phe
				245					250					255	
Arg	Trp	Leu	Ser	Leu	Gly	Ser	Phe	Leu	Ala	Ile	Val	Gly	Ile	Leu	Leu
		260						265					270		
Ala	Gly	Val	Gly	Leu	Asn	Phe	Tyr	Phe	Thr	Leu	Phe	Ala	Ala	Phe	Ser
		275					280					285			
Ser	Tyr	Gly	Ala	Val	Gly	Ser	Leu	Leu	Ala	Val	Phe	Ile	Ala	Leu	Trp
	290					295					300				
Val	Phe	Asn	Ile	Cys	Leu	Ile	Ile	Gly	Leu	Lys	Ile	Asp	Val	Glu	Ile
305					310					315					320
Ser	Arg	Ala	Lys	Gln	Leu	Gln	Ala	Gly	Met	Pro	Ala	Glu	Asp	Tyr	Ser
				325					330					335	
Leu	Val	Pro	Pro	Arg	Ser	Ile	Glu	Lys	Val	Ala	Lys	Met	Lys	Gln	Arg
		340						345					350		
Gln	Gln	Arg	Leu	Met	Asp	Gln	Ala	Ala	Ala	Ile	Arg	Glu	Glu	Ser	Asn
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<211> 717

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(694)

<223> RXA01972

<400> 321

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Val Ala Thr Gly Leu
1 5

ctg tgc ggc att ggt ctg ttt atc gcc acc aat atc gac gac atc atc 163
Leu Ser Ala Ile Gly Leu Phe Ile Ala Thr Asn Ile Asp Asp Ile Ile
10 15 20

gtg ctc tgc ctg ttt ttt gcc cgc ggg gcg ggg caa aaa ggg acc acg 211
Val Leu Ser Leu Phe Phe Ala Arg Gly Ala Gly Gln Lys Gly Thr Thr
25 30 35

ctt cgg att ctg gct ggt cag tac ctc ggc ttc atg ggc atc ctc gcg 259
Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe Met Gly Ile Leu Ala
40 45 50

gcc gca gtc ctg gtc acg ctg ggg gca gga gca ttc cta cct gct gag 307
Ala Ala Val Leu Val Thr Leu Gly Ala Gly Ala Phe Leu Pro Ala Glu
55 60 65

gcg atc ccg tac ttc gga cta att ccc ctg gcc ctg gga cta tgg gcg 355
Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala Leu Gly Leu Trp Ala
70 75 80 85

gcc tgg cag gcc tgg cga agc gat gat gac gac gat gat gat gcg gag 403
Ala Trp Gln Ala Trp Arg Ser Asp Asp Asp Asp Asp Asp Ala Glu
90 95 100

atc gcc ggg aaa aag gtg ggt gtg ctg acc gtc gcc ggt gtg acg ttt 451
Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val Ala Gly Val Thr Phe
105 110 115

gcc aac ggt ggc gac aat atc ggc gtc tac gtc ccg gtc ttc ctc aac 499
Ala Asn Gly Gly Asp Asn Ile Gly Val Tyr Val Pro Val Phe Leu Asn
120 125 130

gtg gac act gcc gcc gtc atc atc tac tgc atc gtt ttc ctc gtc ctg 547
Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile Val Phe Leu Val Leu
135 140 145

gtg gca ggc ctg gtc ctg ctg gca aag ttc gtg gcc acc cgc ccg ccc 595
Val Ala Gly Leu Val Leu Leu Ala Lys Phe Val Ala Thr Arg Pro Pro
150 155 160 165

atc gca gaa gtc ctt gag cgc tgg gag cac gtg ctg ttc ccg atc gtc 643
Ile Ala Glu Val Leu Glu Arg Trp Glu His Val Leu Phe Pro Ile Val
170 175 180

ctg atc ggc ctg ggc atc ttc atc ctc gtc agc ggc ggc gcc ttc ggc 691
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<210> 322

<211> 198

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 322

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Gln Lys Gly Thr Thr Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe
 35 40 45

Met Gly Ile Leu Ala Ala Ala Val Leu Val Thr Leu Gly Ala Gly Ala
 50 55 60

Phe Leu Pro Ala Glu Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala
 65 70 75 80

Leu Gly Leu Trp Ala Ala Trp Gln Ala Trp Arg Ser Asp Asp Asp Asp
 85 90 95

Asp Asp Asp Ala Glu Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val
 100 105 110

Ala Gly Val Thr Phe Ala Asn Gly Gly Asp Asn Ile Gly Val Tyr Val
 115 120 125

Pro Val Phe Leu Asn Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile
 130 135 140

Val Phe Leu Val Leu Val Ala Gly Leu Val Leu Leu Ala Lys Phe Val
 145 150 155 160

Ala Thr Arg Pro Pro Ile Ala Glu Val Leu Glu Arg Trp Glu His Val
 165 170 175

Leu Phe Pro Ile Val Leu Ile Gly Leu Gly Ile Phe Ile Leu Val Ser
 180 185 190

Gly Gly Ala Phe Gly Leu
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<210> 323

<211> 978

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(955)

<223> RXA00311

<400> 323

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		Met Glu His Ser Pro	
		1 5	
gaa ggc aag cgt gga ttc ttc acc tca tgc gtg atg gcg ggt tgc tca			163
Glu Gly Lys Arg Gly Phe Phe Thr Ser Ser Val Met Ala Gly Cys Ser			
	10 15 20		
gtt gga aac gtc ctg gct ggc ttg gta ttt atc ccg ttc ttg atg ctg			211
Val Gly Asn Val Leu Ala Gly Leu Val Phe Ile Pro Phe Leu Met Leu			
	25 30 35		
ccg gaa gaa cac ctc atg tca tgg ggc tgg cgc gta cct ttc ctg ctt			259
Pro Glu Glu His Leu Met Ser Trp Gly Trp Arg Val Pro Phe Leu Leu			
	40 45 50		
tcc gca ctg gtt tta gtt gtc gca tac ttc gtg cgc acc cga ctg gag			307
Ser Ala Leu Val Leu Val Val Ala Tyr Phe Val Arg Thr Arg Leu Glu			
	55 60 65		
gaa gca tca act gag aag gcc gaa gag gac gca ggc gct ccg gct ttg			355
Glu Ala Ser Thr Glu Lys Ala Glu Glu Asp Ala Gly Ala Pro Ala Leu			
	70 75 80 85		
gct gtg ctg cgc acc cag ggc att gat gtc gca cga gtt ttc ctg atc			403
Ala Val Leu Arg Thr Gln Gly Ile Asp Val Ala Arg Val Phe Leu Ile			
	90 95 100		
acc ttc ttc gcc gtt gtt cag acc act ttc aac gtt tac gca ctg gca			451
Thr Phe Phe Ala Val Val Gln Thr Thr Phe Asn Val Tyr Ala Leu Ala			
	105 110 115		
tac gcc gcc aac gaa atc ggc atc gat cgt tcc ttc atg gtg atg gtg			499
Tyr Ala Ala Asn Glu Ile Gly Ile Asp Arg Ser Phe Met Val Met Val			
	120 125 130		
aac acc atc gcg ctg ggg ctt tcc atc gga acg att cct ttg gcc gcg			547
Asn Thr Ile Ala Leu Gly Leu Ser Ile Gly Thr Ile Pro Leu Ala Ala			
	135 140 145		
tgg gtc tct gac cgc att ggc cgc aag cca gtc ttg ctg ttc ggg gcc			595
Trp Val Ser Asp Arg Ile Gly Arg Lys Pro Val Leu Leu Phe Gly Ala			
	150 155 160 165		
atc acc tgt gca atc acc acc tac ttc tac ttc cag gca atc tct gaa			643
Ile Thr Cys Ala Ile Thr Thr Tyr Phe Tyr Phe Gln Ala Ile Ser Glu			
	170 175 180		
gct gac ctt gtg ctg atc ttc gca ctg tgc ttg gtc aac caa ggt ttg			691
Ala Asp Leu Val Leu Ile Phe Ala Leu Cys Leu Val Asn Gln Gly Leu			
	185 190 195		
ttc tac tcc tgc tgg aac ggc gtg tgg acc att ttc ttc cca gaa atg			739
Phe Tyr Ser Cys Trp Asn Gly Val Trp Thr Ile Phe Phe Pro Glu Met			
	200 205 210		
ttc gca tct tcc gtg cgc tac acc ggc atg gct atg ggc aac cag ctc			787
Phe Ala Ser Ser Val Arg Tyr Thr Gly Met Ala Met Gly Asn Gln Leu			
	215 220 225		
ggt ctg atc atc gtt ggt ttc gca cca acc atc gcc acc gcc ctg tac			835

Gly Leu Ile Ile Val Gly Phe Ala Pro Thr Ile Ala Thr Ala Leu Tyr
 230 235 240 245

gca tgg aac ggt tgg gaa gct gtt gcg gga ttc atc atc ggc gca atc 883
 Ala Trp Asn Gly Trp Glu Ala Val Ala Gly Phe Ile Ile Gly Ala Ile
 250 255 260

gca ctg tct gcc gca gtt att ttg acc acc aag gaa acc gcc ttc acc 931
 Ala Leu Ser Ala Ala Val Ile Leu Thr Thr Lys Glu Thr Ala Phe Thr
 265 270 275

aag ctt gaa gat cta ggg aag aaa taatgtctga caagatctgg aaa 978
 Lys Leu Glu Asp Leu Gly Lys Lys
 280 285

<210> 324

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

Met Glu His Ser Pro Glu Gly Lys Arg Gly Phe Phe Thr Ser Ser Val
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 20 25 30

Pro Phe Leu Met Leu Pro Glu Glu His Leu Met Ser Trp Gly Trp Arg
 35 40 45

Val Pro Phe Leu Leu Ser Ala Leu Val Leu Val Val Ala Tyr Phe Val
 50 55 60

Arg Thr Arg Leu Glu Glu Ala Ser Thr Glu Lys Ala Glu Glu Asp Ala
 65 70 75 80

Gly Ala Pro Ala Leu Ala Val Leu Arg Thr Gln Gly Ile Asp Val Ala
 85 90 95

Arg Val Phe Leu Ile Thr Phe Phe Ala Val Val Gln Thr Thr Phe Asn
 100 105 110

Val Tyr Ala Leu Ala Tyr Ala Ala Asn Glu Ile Gly Ile Asp Arg Ser
 115 120 125

Phe Met Val Met Val Asn Thr Ile Ala Leu Gly Leu Ser Ile Gly Thr
 130 135 140

Ile Pro Leu Ala Ala Trp Val Ser Asp Arg Ile Gly Arg Lys Pro Val
 145 150 155 160

Leu Leu Phe Gly Ala Ile Thr Cys Ala Ile Thr Thr Tyr Phe Tyr Phe
 165 170 175

Gln Ala Ile Ser Glu Ala Asp Leu Val Leu Ile Phe Ala Leu Cys Leu
 180 185 190

Val Asn Gln Gly Leu Phe Tyr Ser Cys Trp Asn Gly Val Trp Thr Ile
 195 200 205

549 aqa

<213> Corynebacterium glutamicum

Gly Ile Trp Ala Thr Val Leu Leu Met Ile Ala Arg Ile Ala
130 135 140

<213> Corynebacterium glutamicum

<223> RXN01411

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Met Leu Gly Val Gly
1 5

tgg cgc att cca ttc ctg atg gcc gtg cca cta ggg ctt atc ggc tgg	163
Trp Arg Ile Pro Phe Leu Met Ala Val Pro Leu Gly Leu Ile Gly Trp	
10 15 20	
tgg atc cgc acc ggt gcc cag gaa aat gta cgc ccc gca tcc gaa cgc	211
Trp Ile Arg Thr Gly Ala Gln Glu Asn Val Arg Pro Ala Ser Glu Arg	
25 30 35	
ccc gaa gct cct att aag cag gca ttg cgt act gag tgg aag atg atg	259
Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr Glu Trp Lys Met Met	
40 45 50	
ttg cgg gta ggt ggc ttt atc tct tgc acc ggt ctg agc ttc tac att	307
Leu Arg Val Gly Gly Phe Ile Ser Cys Thr Gly Leu Ser Phe Tyr Ile	
55 60 65	
ttc acc acg tac atg acc act ttc ctg cgc agc acc gtc gga ctg gag	355
Phe Thr Thr Tyr Met Thr Thr Phe Leu Arg Ser Thr Val Gly Leu Glu	
70 75 80 85	
ggc acg tta gtg ctg gct gga aac atc atc gct ctc agc atg gca gca	403
Gly Thr Leu Val Leu Ala Gly Asn Ile Ile Ala Leu Ser Met Ala Ala	
90 95 100	
att gtg gcc cca ttt gtt ggc cgc gca att gat aaa ttc ccc cgc cgg	451
Ile Val Ala Pro Phe Val Gly Arg Ala Ile Asp Lys Phe Pro Arg Arg	
105 110 115	
aac atc atg gct ttc gct acc tta agc aca gta att atg gcg atc ccg	499
Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val Ile Met Ala Ile Pro	
120 125 130	
gcc tac atc att gca ggt caa ggt act ttg act gct tct ttg att gcg	547
Ala Tyr Ile Ile Ala Gly Gln Gly Thr Leu Thr Ala Ser Leu Ile Ala	
135 140 145	
cag gta atg ctt gga atc ggc gcg gtt acc gct aac tgc gtt acc tca	595
Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys Val Thr Ser	
150 155 160 165	
gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt act tcc gcc	643
Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly Thr Ser Ala	
170 175 180	
ggc att acc tac aac gtc act tac gca atc ttc ggc ggc tcg gct cca	691
Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly Ser Ala Pro	
185 190 195	
ttt atc tcc acc gca ttg gtc tcc tgg acc ggc agc ccg ctg gcc cct	739
Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro Leu Ala Pro	
200 205 210	
gcg gta tac atg atc atc att gcg ctc ttc gcc ttc acc gcg tcc cgc	787
Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr Ala Ser Arg	
215 220 225	
ttc att cct gaa acc tcc cca gtt ttt gtc acc gca acc ccg gcc att	835
Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr Pro Ala Ile	
230 235 240 245	

aag gca cca aag gtg ctg gtc aac ccg ggt taaaccacgc ttttcgacga 885
 Lys Ala Pro Lys Val Leu Val Asn Pro Gly
 250 255

aaa 888

<210> 328

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

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Pro Ala Ser Glu Arg Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr
 35 40 45

Glu Trp Lys Met Met Leu Arg Val Gly Gly Phe Ile Ser Cys Thr Gly
 50 55 60

Leu Ser Phe Tyr Ile Phe Thr Thr Tyr Met Thr Thr Phe Leu Arg Ser
 65 70 75 80

Thr Val Gly Leu Glu Gly Thr Leu Val Leu Ala Gly Asn Ile Ile Ala
 85 90 95

Leu Ser Met Ala Ala Ile Val Ala Pro Phe Val Gly Arg Ala Ile Asp
 100 105 110

Lys Phe Pro Arg Arg Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val
 115 120 125

Ile Met Ala Ile Pro Ala Tyr Ile Ile Ala Gly Gln Gly Thr Leu Thr
 130 135 140

Ala Ser Leu Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala
 145 150 155 160

Asn Cys Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr
 165 170 175

Arg Gly Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe
 180 185 190

Gly Gly Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly
 195 200 205

Ser Pro Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala
 210 215 220

Phe Thr Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr
 225 230 235 240

Ala Thr Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly
 245 250 255

<210> 329
 <211> 350
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(327)
 <223> FRXA01411

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 gtt acc tca gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt 96
 Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly
 20 25 30
 act tcc gcc ggc att acc tac aac gtc act tac gca atc ttc ggc ggc 144
 Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly
 35 40 45
 tcg gct cca ttt atc tcc acc gca ttg gtc tcc tgg acc ggc agc ccg 192
 Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro
 50 55 60
 ctg gcc cct gcg gta tac atg atc atc att gcg ctc ttc gcc ttc acc 240
 Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr
 65 70 75 80
 gcg tcc cgc ttc att cct gaa acc tcc cca gtt ttt gtc acc gca acc 288
 Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr
 85 90 95
 ccg gcc att aag gca cca aag gtg ctg gtc aac ccg ggt taaaccacgc 337
 Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly
 100 105
 ttttcgacga aaa 350

<210> 330
 <211> 109
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 330
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 20 25 30
 Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly
 35 40 45
 Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro
 50 55 60

Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly
100 105

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<223> RXA01900
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Met Thr Thr Ala Val																	5
1																	
gat caa aac tca ccg ccc aag cag caa ctc aac aag cgc gtc ctg ctg																	163
Asp Gln Asn Ser Pro Pro Lys Gln Gln Leu Asn Lys Arg Val Leu Leu																	
10 15 20																	
ggc agc ttg agt ggc agc gtt atc gaa tgg ttc gac ttc ctg gtt tac																	211
Gly Ser Leu Ser Gly Ser Val Ile Glu Trp Phe Asp Phe Leu Val Tyr																	
25 30 35																	
gga acc gtc gcc gcg ctg gtc ttc aac aag atg tac ttc ccc agc ggc																	259
Gly Thr Val Ala Ala Leu Val Phe Asn Lys Met Tyr Phe Pro Ser Gly																	
40 45 50																	
aac gag ttc ctc tcc aca atc ctg gcg tac gca tcc ttc tcc ctg acc																	307
Asn Glu Phe Leu Ser Thr Ile Leu Ala Tyr Ala Ser Phe Ser Leu Thr																	
55 60 65																	
ttc ttc ttc cgc ccc att ggt ggc gtc atc ttc gcc cac atc ggc gac																	355
Phe Phe Phe Arg Pro Ile Gly Gly Val Ile Phe Ala His Ile Gly Asp																	
70 75 80 85																	
cgc att ggg cgt aag aag acc ctg ttc atc acc ttg atg ctc atg ggt																	403
Arg Ile Gly Arg Lys Lys Thr Leu Phe Ile Thr Leu Met Leu Met Gly																	
90 95 100																	
ggc ggc acc gtc gcc att ggt ttg ctg ccc gac tac aac gcc atc ggc																	451
Gly Gly Thr Val Ala Ile Gly Leu Leu Pro Asp Tyr Asn Ala Ile Gly																	
105 110 115																	
att tgg gca cca atc ctt ctg atg ttc ctc cgc att ttg cag ggc atc																	499
Ile Trp Ala Pro Ile Leu Leu Met Phe Leu Arg Ile Leu Gln Gly Ile																	
120 125 130																	
gga att ggc ggc gaa tgg ggt ggc gca ctg ctc ctg gca tac gaa tac																	547
Gly Ile Gly Gly Glu Trp Gly Gly Ala Leu Leu Leu Ala Tyr Glu Tyr																	

135	140	145	
gct cca aag aag cag cgt ggg ctc tac ggc gca gtt cct caa atg ggc			595
Ala Pro Lys Lys Gln Arg Gly Leu Tyr Gly Ala Val Pro Gln Met Gly			
150	155	160	165
att tcc ctg ggc atg ctg ctt gca gct ggc gtg atc tct ctg ctc acc			643
Ile Ser Leu Gly Met Leu Leu Ala Ala Gly Val Ile Ser Leu Leu Thr			
170	175		180
ctc atg ccg gaa gat cag ttc ctc acc tgg ggc tgg cgc atc cca ttc			691
Leu Met Pro Glu Asp Gln Phe Leu Thr Trp Gly Trp Arg Ile Pro Phe			
185	190		195
gtc gga tcc atc ctc cta gtg ttc atc ggc ctg ttc atc cga aac ggc			739
Val Gly Ser Ile Leu Leu Val Phe Ile Gly Leu Phe Ile Arg Asn Gly			
200	205		210
ctt gat gaa acc ccc gag ttc aag cgt atc cgc gat tcc ggc cag cag			787
Leu Asp Glu Thr Pro Glu Phe Lys Arg Ile Arg Asp Ser Gly Gln Gln			
215	220		225
gta aag atg cct ctg aag gaa gtt ctg acc aag tac tgg cca gcc gtt			835
Val Lys Met Pro Leu Lys Glu Val Leu Thr Lys Tyr Trp Pro Ala Val			
230	235		245
ctg gtc tcc atc ggc gca aaa gct gcc gag acc ggc ccc ttc tac atc			883
Leu Val Ser Ile Gly Ala Lys Ala Ala Glu Thr Gly Pro Phe Tyr Ile			
250	255		260
ttc ggc acc tac atc gtt gct tac gca acc aac ttc ctg aac atc cgc			931
Phe Gly Thr Tyr Ile Val Ala Tyr Ala Thr Asn Phe Leu Asn Ile Arg			
265	270		275
gac aac att gtc ctt ctg gca gtt gct tgc gcc gcc ctc gtt gcc acc			979
Asp Asn Ile Val Leu Leu Ala Val Ala Cys Ala Ala Leu Val Ala Thr			
280	285		290
atc tgg atg cca ctg ttc gga tcc ttc tcc gac cgc gtc aac cgt gca			1027
Ile Trp Met Pro Leu Phe Gly Ser Phe Ser Asp Arg Val Asn Arg Ala			
295	300		305
gtg ctc tac agg atc tgt gca tcc gca acc atc gtg ctg att gtc cct			1075
Val Leu Tyr Arg Ile Cys Ala Ser Ala Thr Ile Val Leu Ile Val Pro			
310	315		325
tac tac ttg gtc ctc aac acc ggc gaa att tgg gca ctg ttt atc act			1123
Tyr Tyr Leu Val Leu Asn Thr Gly Glu Ile Trp Ala Leu Phe Ile Thr			
330	335		340
acc gtg att ggc ttc ggc atc ctc tgg ggt agc gtc aac gca atc ctc			1171
Thr Val Ile Gly Phe Gly Ile Leu Trp Gly Ser Val Asn Ala Ile Leu			
345	350		355
gga acc gtc atc gca gaa aac ttc gca cct gag gtc cgc tac acc ggc			1219
Gly Thr Val Ile Ala Glu Asn Phe Ala Pro Glu Val Arg Tyr Thr Gly			
360	365		370
gct acc ctg ggt tac caa gtc gga gca gca ctc ttc ggc ggt acc gca			1267
Ala Thr Leu Gly Tyr Gln Val Gly Ala Ala Leu Phe Gly Gly Thr Ala			
375	380		385

ccc att atc gca gca tgg ctg ttc gaa atc tcc ggc gga caa tgg tgg 1315
 Pro Ile Ile Ala Ala Trp Leu Phe Glu Ile Ser Gly Gly Gln Trp Trp
 390 395 400 405

cca atc gcc gtc tac gtc gct gca tgt tgc ctt ctc tct gtg atc gcc 1363
 Pro Ile Ala Val Tyr Val Ala Ala Cys Cys Leu Leu Ser Val Ile Ala
 410 415 420

tcg ttc ttc atc caa cgc gtc gcg cac caa gag aac taaaatctaa 1409
 Ser Phe Phe Ile Gln Arg Val Ala His Gln Glu Asn
 425 430

gtaaaacccc tcc 1422

<210> 332

<211> 433

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

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 20 25 30

Asp Phe Leu Val Tyr Gly Thr Val Ala Ala Leu Val Phe Asn Lys Met
 35 40 45

Tyr Phe Pro Ser Gly Asn Glu Phe Leu Ser Thr Ile Leu Ala Tyr Ala
 50 55 60

Ser Phe Ser Leu Thr Phe Phe Phe Arg Pro Ile Gly Gly Val Ile Phe
 65 70 75 80

Ala His Ile Gly Asp Arg Ile Gly Arg Lys Lys Thr Leu Phe Ile Thr
 85 90 95

Leu Met Leu Met Gly Gly Gly Thr Val Ala Ile Gly Leu Leu Pro Asp
 100 105 110

Tyr Asn Ala Ile Gly Ile Trp Ala Pro Ile Leu Leu Met Phe Leu Arg
 115 120 125

Ile Leu Gln Gly Ile Gly Ile Gly Gly Glu Trp Gly Gly Ala Leu Leu
 130 135 140

Leu Ala Tyr Glu Tyr Ala Pro Lys Lys Gln Arg Gly Leu Tyr Gly Ala
 145 150 155 160

Val Pro Gln Met Gly Ile Ser Leu Gly Met Leu Leu Ala Ala Gly Val
 165 170 175

Ile Ser Leu Leu Thr Leu Met Pro Glu Asp Gln Phe Leu Thr Trp Gly
 180 185 190

Trp Arg Ile Pro Phe Val Gly Ser Ile Leu Leu Val Phe Ile Gly Leu
 195 200 205

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Phe Ile Arg Asn Gly Leu Asp Glu Thr Pro Glu Phe Lys Arg Ile Arg
 210                      215                      220

Asp Ser Gly Gln Gln Val Lys Met Pro Leu Lys Glu Val Leu Thr Lys
225                      230                      235                      240

Tyr Trp Pro Ala Val Leu Val Ser Ile Gly Ala Lys Ala Ala Glu Thr
                245                      250                      255

Gly Pro Phe Tyr Ile Phe Gly Thr Tyr Ile Val Ala Tyr Ala Thr Asn
                260                      265                      270

Phe Leu Asn Ile Arg Asp Asn Ile Val Leu Leu Ala Val Ala Cys Ala
                275                      280                      285

Ala Leu Val Ala Thr Ile Trp Met Pro Leu Phe Gly Ser Phe Ser Asp
 290                      295                      300

Arg Val Asn Arg Ala Val Leu Tyr Arg Ile Cys Ala Ser Ala Thr Ile
305                      310                      315                      320

Val Leu Ile Val Pro Tyr Tyr Leu Val Leu Asn Thr Gly Glu Ile Trp
                325                      330                      335

Ala Leu Phe Ile Thr Thr Val Ile Gly Phe Gly Ile Leu Trp Gly Ser
                340                      345                      350

Val Asn Ala Ile Leu Gly Thr Val Ile Ala Glu Asn Phe Ala Pro Glu
 355                      360                      365

Val Arg Tyr Thr Gly Ala Thr Leu Gly Tyr Gln Val Gly Ala Ala Leu
 370                      375                      380

Phe Gly Gly Thr Ala Pro Ile Ile Ala Ala Trp Leu Phe Glu Ile Ser
385                      390                      395                      400

Gly Gly Gln Trp Trp Pro Ile Ala Val Tyr Val Ala Ala Cys Cys Leu
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Leu Ser Val Ile Ala Ser Phe Phe Ile Gln Arg Val Ala His Gln Glu
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Asn

<210> 333

<211> 1524

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1501)

<223> RXA02507

<400> 333

attaccacaca atttcaatcg gtttatacaa ccagcctcta actggcaaca ggactgcaga 60

cagaaactgt tgctggaacc ttcatgaac aggatcgaca atg agc gaa caa ctt 115
 Met Ser Glu Gln Leu

															1	5	
cag ggt gta act cac tcc gaa tca act ccg ggc aag acg ccc aag cga	163																
Gln Gly Val Thr His Ser Glu Ser Thr Pro Gly Lys Thr Pro Lys Arg																	
10 15 20																	
gca gca cta tcc agc tgg atc ggc tca gct ctc gaa tac tac gac ttc	211																
Ala Ala Leu Ser Ser Trp Ile Gly Ser Ala Leu Glu Tyr Tyr Asp Phe																	
25 30 35																	
gct gtt tac gga acc gct gca gcg ctg gtt ctt aac cac ctc ttc ttc	259																
Ala Val Tyr Gly Thr Ala Ala Ala Leu Val Leu Asn His Leu Phe Phe																	
40 45 50																	
cca gct gat act tca cca ggc atc gca att ttg gct gcg atg ggt acc	307																
Pro Ala Asp Thr Ser Pro Gly Ile Ala Ile Leu Ala Ala Met Gly Thr																	
55 60 65																	
gtg ggt gtt gct tat gtg gtt cgc cct ctt ggt gcg ctg atc atg ggt	355																
Val Gly Val Ala Tyr Val Val Arg Pro Leu Gly Ala Leu Ile Met Gly																	
70 75 80 85																	
cca tta ggt gac cgt tac gga cgt aaa ttt gtc ctc atg ctg tgc ctc	403																
Pro Leu Gly Asp Arg Tyr Gly Arg Lys Phe Val Leu Met Leu Cys Leu																	
90 95 100																	
ttc ctg att gga gca tcc act ttc gca gtt ggc tgc ttg cca aca ttt	451																
Phe Leu Ile Gly Ala Ser Thr Phe Ala Val Gly Cys Leu Pro Thr Phe																	
105 110 115																	
gat cag gtc ggt tac ttg gct ccg gca ctg ttg gtg ctg tgc cgt gtg	499																
Asp Gln Val Gly Tyr Leu Ala Pro Ala Leu Leu Val Leu Cys Arg Val																	
120 125 130																	
atc cag gga ctg tct gca tcc ggt gag cag tcc agt gcg att tcc gtt	547																
Ile Gln Gly Leu Ser Ala Ser Gly Glu Gln Ser Ser Ala Ile Ser Val																	
135 140 145																	
tct ttg gag cac gcc gat gag cgt cac cgc gca ttt act gct agc tgg	595																
Ser Leu Glu His Ala Asp Glu Arg His Arg Ala Phe Thr Ala Ser Trp																	
150 155 160 165																	
act ctt cac gga acc cag ttc ggt acc ttg ctg gca acc gga gta ttt	643																
Thr Leu His Gly Thr Gln Phe Gly Thr Leu Leu Ala Thr Gly Val Phe																	
170 175 180																	
atc cca ttc acc ttg ttc ctg agt gaa gat gct cta atg tca tgg ggt	691																
Ile Pro Phe Thr Leu Phe Leu Ser Glu Asp Ala Leu Met Ser Trp Gly																	
185 190 195																	
tgg cgc gtt ccg ttc tgg ctg tcc gct gct gtt gtt ttg gtt gct ttc	739																
Trp Arg Val Pro Phe Trp Leu Ser Ala Ala Val Val Leu Val Ala Phe																	
200 205 210																	
ctc atc cgt cgt gga ctg gaa gag cca cca gca ttc cgt gaa aac aag	787																
Leu Ile Arg Arg Gly Leu Glu Glu Pro Pro Ala Phe Arg Glu Asn Lys																	
215 220 225																	
gaa gca gtt gca gcc gca gca tct cca ctg gcg atg acc ttg cgt tac	835																
Glu Ala Val Ala Gly Ala Ala Ser Pro Leu Ala Met Thr Leu Arg Tyr																	
230 235 240 245																	

cac aag gcg gcg gtt gct cgc gtt gct att gct gcg atg atc aac tcc 883
 His Lys Ala Ala Val Ala Arg Val Ala Ile Ala Ala Met Ile Asn Ser
 250 255 260

gtg aac att gtg ttt act gtg tgg gca ctg tcg ttc gcc acc aac att 931
 Val Asn Ile Val Phe Thr Val Trp Ala Leu Ser Phe Ala Thr Asn Ile
 265 270 275

gtt ggc ctg gat cgt tca act gtt ttg ctg gtt cca gtt gtt gcg aac 979
 Val Gly Leu Asp Arg Ser Thr Val Leu Leu Val Pro Val Val Ala Asn
 280 285 290

ttg gtt gca ctg att gcg att cct ttg tcc gcc atg ctg gct gac cgc 1027
 Leu Val Ala Leu Ile Ala Ile Pro Leu Ser Gly Met Leu Ala Asp Arg
 295 300 305

att ggt cgc cga cca gtg ttc atc atg ggt gcc att ggt ggt ggc ctg 1075
 Ile Gly Arg Arg Pro Val Phe Ile Met Gly Ala Ile Gly Gly Gly Leu
 310 315 320 325

gcc atg aac ggt tac ctg gga gct atc tac tcc gcc aat tgg acc atg 1123
 Ala Met Asn Gly Tyr Leu Gly Ala Ile Tyr Ser Gly Asn Trp Thr Met
 330 335 340

atc ttc ttc atg ggc gtg ttg atg tct ggt ctg ctg tac tcc atg ggt 1171
 Ile Phe Phe Met Gly Val Leu Met Ser Gly Leu Leu Tyr Ser Met Gly
 345 350 355

aat gcc gtg tgg cca gcg ttc tac gca gaa atg ttc cca acc tct gtg 1219
 Asn Ala Val Trp Pro Ala Phe Tyr Ala Glu Met Phe Pro Thr Ser Val
 360 365 370

cgt gtc acc ggc ttg gct ctt gga act cag att ggt ttc gca gtc tct 1267
 Arg Val Thr Gly Leu Ala Leu Gly Thr Gln Ile Gly Phe Ala Val Ser
 375 380 385

ggt ggt ttc gtc cca gtt atc gca tcc gcg ctt gct ggt gat cag ggt 1315
 Gly Gly Phe Val Pro Val Ile Ala Ser Ala Leu Ala Gly Asp Gln Gly
 390 395 400 405

gac cag tgg atg aag gtg tcc atc ttc gtt ggt gtt gtt tgt gtg att 1363
 Asp Gln Trp Met Lys Val Ser Ile Phe Val Gly Val Val Cys Val Ile
 410 415 420

tct gca ctg gtt gcc atg acc gct aag gaa acc aag gct ctg act ctg 1411
 Ser Ala Leu Val Ala Met Thr Ala Lys Glu Thr Lys Ala Leu Thr Leu
 425 430 435

gat gag atc gat gct ctg cac act gct ggt ggt gag gcc gca gac ctg 1459
 Asp Glu Ile Asp Ala Leu His Thr Ala Gly Gly Glu Ala Ala Asp Leu
 440 445 450

gca gcc gca agc aaa gcc tcc gag gcc caa ctc gcg gct cag 1501
 Ala Ala Ala Ser Lys Ala Ser Glu Ala Gln Leu Ala Ala Gln
 455 460 465

taaaacaaaa aggaatcttt gac 1524

<213> Corynebacterium glutamicum

Met Ser Glu Gln Leu Gln Gly Val Thr His Ser Glu Ser Thr Pro Gly
1 5 10 15

Lys Thr Pro Lys Arg Ala Ala Leu Ser Ser Trp Ile Gly Ser Ala Leu
20 25 30

Glu Tyr Tyr Asp Phe Ala Val Tyr Gly Thr Ala Ala Ala Leu Val Leu
35 40 45

Asn His Leu Phe Phe Pro Ala Asp Thr Ser Pro Gly Ile Ala Ile Leu
50 55 60

Ala Ala Met Gly Thr Val Gly Val Ala Tyr Val Val Arg Pro Leu Gly
65 70 75 80

Ala Leu Ile Met Gly Pro Leu Gly Asp Arg Tyr Gly Arg Lys Phe Val
85 90 95

Leu Met Leu Cys Leu Phe Leu Ile Gly Ala Ser Thr Phe Ala Val Gly
100 105 110

Cys Leu Pro Thr Phe Asp Gln Val Gly Tyr Leu Ala Pro Ala Leu Leu
115 120 125

Val Leu Cys Arg Val Ile Gln Gly Leu Ser Ala Ser Gly Glu Gln Ser
130 135 140

Ser Ala Ile Ser Val Ser Leu Glu His Ala Asp Glu Arg His Arg Ala
145 150 155 160

Phe Thr Ala Ser Trp Thr Leu His Gly Thr Gln Phe Gly Thr Leu Leu
165 170 175

Ala Thr Gly Val Phe Ile Pro Phe Thr Leu Phe Leu Ser Glu Asp Ala
180 185 190

Leu Met Ser Trp Gly Trp Arg Val Pro Phe Trp Leu Ser Ala Ala Val
195 200 205

Val Leu Val Ala Phe Leu Ile Arg Arg Gly Leu Glu Glu Pro Pro Ala
210 215 220

Phe Arg Glu Asn Lys Glu Ala Val Ala Gly Ala Ala Ser Pro Leu Ala
225 230 235 240

Met Thr Leu Arg Tyr His Lys Ala Ala Val Ala Arg Val Ala Ile Ala
245 250 255

Ala Met Ile Asn Ser Val Asn Ile Val Phe Thr Val Trp Ala Leu Ser
260 265 270

Phe Ala Thr Asn Ile Val Gly Leu Asp Arg Ser Thr Val Leu Leu Val
275 280 285

Pro Val Val Ala Asn Leu Val Ala Leu Ile Ala Ile Pro Leu Ser Gly
290 295 300[illegible]

Met Leu Ala Asp Arg Ile Gly Arg Arg Pro Val Phe Ile Met Gly Ala
305 310 315 320

Ile Gly Gly Gly Leu Ala Met Asn Gly Tyr Leu Gly Ala Ile Tyr Ser
325 330 335

Gly Asn Trp Thr Met Ile Phe Phe Met Gly Val Leu Met Ser Gly Leu
340 345 350

Leu Tyr Ser Met Gly Asn Ala Val Trp Pro Ala Phe Tyr Ala Glu Met
355 360 365

Phe Pro Thr Ser Val Arg Val Thr Gly Leu Ala Leu Gly Thr Gln Ile
370 375 380

Gly Phe Ala Val Ser Gly Gly Phe Val Pro Val Ile Ala Ser Ala Leu
385 390 395 400

Ala Gly Asp Gln Gly Asp Gln Trp Met Lys Val Ser Ile Phe Val Gly
405 410 415

Val Val Cys Val Ile Ser Ala Leu Val Ala Met Thr Ala Lys Glu Thr
420 425 430

Lys Ala Leu Thr Leu Asp Glu Ile Asp Ala Leu His Thr Ala Gly Gly
435 440 445

Glu Ala Ala Asp Leu Ala Ala Ala Ser Lys Ala Ser Glu Ala Gln Leu
450 455 460

Ala Ala Gln
465

<210> 335

<211> 955

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (21)..(932)

<223> RXA00445

<400> 335

ggtgcaaaaa aggactaacc atg gcg gat ctg agc att gaa cac gta tca agg 53
Met Ala Asp Leu Ser Ile Glu His Val Ser Arg
1 5 10

ttt ttc ggc gat gcc atc gcc ttg aac gat gtg tca ttg acc gtc ccc 101
Phe Phe Gly Asp Ala Ile Ala Leu Asn Asp Val Ser Leu Thr Val Pro
15 20 25

tca ggc tcc atc acc gcc atc atc ggg ccg tcc ggg agc ggt aaa acc 149
Ser Gly Ser Ile Thr Ala Ile Ile Gly Pro Ser Gly Ser Gly Lys Thr
30 35 40

acg tta ctg cgt ttg ctg gca ggc ctt gat tca ccc gat gaa ggc acc 197
Thr Leu Leu Arg Leu Leu Ala Gly Leu Asp Ser Pro Asp Glu Gly Thr
45 50 55

gtg agc att ggg aat aag atc gcc aag ctg ggt gac act gcg ctg tgt 245
 Val Ser Ile Gly Asn Lys Ile Ala Lys Leu Gly Asp Thr Ala Leu Cys
 60 65 70 75

ttc cag gat tcg cct ttg tat ccg cac ctt aat gtg tgg gaa aac gtg 293
 Phe Gln Asp Ser Pro Leu Tyr Pro His Leu Asn Val Trp Glu Asn Val
 80 85 90

gca ttt ccg ctc aag ctc aaa gcc acc aat act gca gat gag gtg gtg 341
 Ala Phe Pro Leu Lys Leu Lys Ala Thr Asn Thr Ala Asp Glu Val Val
 95 100 105

aaa aag cgg gtg agt gat gtt ttg gaa atg ctc gaa att gct ccc ctc 389
 Lys Lys Arg Val Ser Asp Val Leu Glu Met Leu Glu Ile Ala Pro Leu
 110 115 120

gcc cgc cgg aaa att acc gaa ctc tcc ggc ggg caa aaa cag cgc gtc 437
 Ala Arg Arg Lys Ile Thr Glu Leu Ser Gly Gly Gln Lys Gln Arg Val
 125 130 135

ggc att gct cga gca ctg gtc aga gac gta gag gtt tac ctt ttc gac 485
 Gly Ile Ala Arg Ala Leu Val Arg Asp Val Glu Val Tyr Leu Phe Asp
 140 145 150 155

gaa ccg atg gcc cac ctc gac caa gcc tta gcc cgc gat att gtg gcc 533
 Glu Pro Met Ala His Leu Asp Gln Ala Leu Ala Arg Asp Ile Val Ala
 160 165 170

gat ctg cgc aaa att caa caa tcg ttg gga ctg acg ttt gta tac gtc 581
 Asp Leu Arg Lys Ile Gln Gln Ser Leu Gly Leu Thr Phe Val Tyr Val
 175 180 185

acc cac agc aaa tcc gag gca ttc gcg ctc gcc gac caa att gtc gtg 629
 Thr His Ser Lys Ser Glu Ala Phe Ala Leu Ala Asp Gln Ile Val Val
 190 195 200

ctg gta gat ggc caa gtc gcg cag gtt ggt gag gcg gag gag ctc gtc 677
 Leu Val Asp Gly Gln Val Ala Gln Val Gly Glu Ala Glu Glu Leu Val
 205 210 215

gaa aag cca aaa acc cta gaa ata gcc gag ttc ctc tcc ccc acc gag 725
 Glu Lys Pro Lys Thr Leu Glu Ile Ala Glu Phe Leu Ser Pro Thr Glu
 220 225 230 235

ctc aat gtg cgc cgg cgt ggg gac gcc gtg gag gca tgg cga ccc gaa 773
 Leu Asn Val Arg Arg Arg Gly Asp Ala Val Glu Ala Trp Arg Pro Glu
 240 245 250

gac acc cag ctc gcc cgc ggt ggc act gcg acc gtg gaa gcc gtg acg 821
 Asp Thr Gln Leu Ala Arg Gly Gly Thr Ala Thr Val Glu Ala Val Thr
 255 260 265

tat ttg ggc cgc gag tgg ctt gta caa acc acc gag ggg cac gcc gtg 869
 Tyr Leu Gly Arg Glu Trp Leu Val Gln Thr Thr Glu Gly His Ala Val
 270 275 280

tcg gag gaa aaa ttc gac gtc ggc gaa agc gtc acg cta acc cag aag 917
 Ser Glu Glu Lys Phe Asp Val Gly Glu Ser Val Thr Leu Thr Gln Lys
 285 290 295

955

<400> 336															
Met 1	Ala	Asp	Leu	Ser 5	Ile	Glu	His	Val	Ser 10	Arg	Phe	Phe	Gly	Asp 15	Ala
Ile	Ala	Leu	Asn 20	Asp	Val	Ser	Leu	Thr 25	Val	Pro	Ser	Gly	Ser 30	Ile	Thr
Ala	Ile	Ile 35	Gly	Pro	Ser	Gly	Ser 40	Gly	Lys	Thr	Thr	Leu 45	Leu	Arg	Leu
Leu	Ala	Gly	Leu	Asp	Ser	Pro 55	Asp	Glu	Gly	Thr	Val 60	Ser	Ile	Gly	Asn
Lys 65	Ile	Ala	Lys	Leu	Gly 70	Asp	Thr	Ala	Leu	Cys 75	Phe	Gln	Asp	Ser	Pro 80
Leu	Tyr	Pro	His	Leu 85	Asn	Val	Trp	Glu	Asn 90	Val	Ala	Phe	Pro	Leu 95	Lys
Leu	Lys	Ala	Thr 100	Asn	Thr	Ala	Asp	Glu 105	Val	Val	Lys	Lys	Arg 110	Val	Ser
Asp	Val	Leu 115	Glu	Met	Leu	Glu	Ile 120	Ala	Pro	Leu	Ala 125	Arg	Arg	Lys	Ile
Thr	Glu 130	Leu	Ser	Gly	Gly	Gln 135	Lys	Gln	Arg	Val	Gly 140	Ile	Ala	Arg	Ala
Leu 145	Val	Arg	Asp	Val	Glu 150	Val	Tyr	Leu	Phe	Asp 155	Glu	Pro	Met	Ala	His 160
Leu	Asp	Gln	Ala 165	Leu	Ala	Arg	Asp	Ile 170	Val	Ala	Asp	Leu	Arg	Lys 175	Ile
Gln	Gln	Ser	Leu 180	Gly	Leu	Thr	Phe	Val 185	Tyr	Val	Thr	His	Ser 190	Lys	Ser
Glu	Ala	Phe 195	Ala	Leu	Ala	Asp	Gln 200	Ile	Val	Val	Leu 205	Val	Asp	Gly	Gln
Val 210	Ala	Gln	Val	Gly	Glu 215	Ala	Glu	Glu	Leu	Val	Glu 220	Lys	Pro	Lys	Thr
Leu 225	Glu	Ile	Ala	Glu	Phe 230	Leu	Ser	Pro	Thr	Glu 235	Leu	Asn	Val	Arg	Arg 240
Arg	Gly	Asp	Ala 245	Val	Glu	Ala	Trp	Arg	Pro 250	Glu	Asp	Thr	Gln	Leu 255	Ala
Arg	Gly	Gly	Thr 260	Ala	Thr	Val	Glu 265	Ala	Val	Thr	Tyr	Leu 270	Gly	Arg	Glu

Trp Leu Val Gln Thr Thr Glu Gly His Ala Val Ser Glu Glu Lys Phe
275 280 285

Asp Val Gly Glu Ser Val Thr Leu Thr Gln Lys Lys Val Phe Ser Phe
290 295 300

<210> 337

<211> 491

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(468)

<223> RXA02353

<400> 337

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Met Ala Leu Leu Ile Leu Ala Gly Leu Gln Met Ile Pro Lys Glu Thr	
1 5 10 15	
tac gaa gca gcc cgc gtc gat ggc gca acc gcg tgg cag caa ttc acc	96
Tyr Glu Ala Ala Arg Val Asp Gly Ala Thr Ala Trp Gln Gln Phe Thr	
20 25 30	
aag atc acc ctc ccg ctg gtg cgc cca gct ttg atg gtg gca gta ctc	144
Lys Ile Thr Leu Pro Leu Val Arg Pro Ala Leu Met Val Ala Val Leu	
35 40 45	
ttc cgc acc ctc gat gcg cta cgc atg tat gac ctc ccc gtc atc atg	192
Phe Arg Thr Leu Asp Ala Leu Arg Met Tyr Asp Leu Pro Val Ile Met	
50 55 60	
atc tcc agc tcc tcc aac tcc ccc acc gct gtt atc tcc cag ctg gtt	240
Ile Ser Ser Ser Ser Asn Ser Pro Thr Ala Val Ile Ser Gln Leu Val	
65 70 75 80	
gtg gaa gac atg cgc caa aac aac ttc aac tcc gct tcc gcc ctt tcc	288
Val Glu Asp Met Arg Gln Asn Asn Phe Asn Ser Ala Ser Ala Leu Ser	
85 90 95	
aca ctg atc ttc ctg ctg atc ttc ttc gtg gcg ttc atc atg atc cga	336
Thr Leu Ile Phe Leu Leu Ile Phe Phe Val Ala Phe Ile Met Ile Arg	
100 105 110	
ttc ctc ggc gca gat gtt tcg ggc caa cgc gga ata aag aaa aag aaa	384
Phe Leu Gly Ala Asp Val Ser Gly Gln Arg Gly Ile Lys Lys Lys Lys	
115 120 125	
ctg ggc gga acc aag gat gag aaa ccc acc gct aag gat gct gtt gta	432
Leu Gly Gly Thr Lys Asp Glu Lys Pro Thr Ala Lys Asp Ala Val Val	
130 135 140	
aag gcc gat tct gct gtg aag gaa gcc gct aag cca tgactaaacg	478
Lys Ala Asp Ser Ala Val Lys Glu Ala Ala Lys Pro	
145 150 155	

aacaaaagga ctc

491

<210> 338

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Ala Leu Leu Ile Leu Ala Gly Leu Gln Met Ile Pro Lys Glu Thr
 1 5 10 15

Tyr Glu Ala Ala Arg Val Asp Gly Ala Thr Ala Trp Gln Gln Phe Thr
 20 25 30

Lys Ile Thr Leu Pro Leu Val Arg Pro Ala Leu Met Val Ala Val Leu
 35 40 45

Phe Arg Thr Leu Asp Ala Leu Arg Met Tyr Asp Leu Pro Val Ile Met
 50 55 60

Ile Ser Ser Ser Ser Asn Ser Pro Thr Ala Val Ile Ser Gln Leu Val
 65 70 75 80

Val Glu Asp Met Arg Gln Asn Asn Phe Asn Ser Ala Ser Ala Leu Ser
 85 90 95

Thr Leu Ile Phe Leu Leu Ile Phe Phe Val Ala Phe Ile Met Ile Arg
 100 105 110

Phe Leu Gly Ala Asp Val Ser Gly Gln Arg Gly Ile Lys Lys Lys Lys
 115 120 125

Leu Gly Gly Thr Lys Asp Glu Lys Pro Thr Ala Lys Asp Ala Val Val
 130 135 140

Lys Ala Asp Ser Ala Val Lys Glu Ala Ala Lys Pro
 145 150 155

<210> 339

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01297

<400> 339

tcctgttgct gctgattatc actgttatcc aggttcgata catggataag gagaacaagc 60

agaaatgata tcgactgata gaaacgtttt ggtcaaaatc atg ggc tat gtc ggc 115
 Met Gly Tyr Val Gly
 1 5

atg gtt ctt gcc atc ttg ttc att ggc ctt ccg ctg gta ttt att gtg 163
 Met Val Leu Ala Ile Leu Phe Ile Gly Leu Pro Leu Val Phe Ile Val
 10 15 20

ctg act agc ttc aag cag cag tca gag att tac acc cag ccg gtc acg	211
Leu Thr Ser Phe Lys Gln Gln Ser Glu Ile Tyr Thr Gln Pro Val Thr	
25 30 35	
tgg ttc cct tcg gaa ttt aat ttc gat aac tat gca aat gtt ttc gag	259
Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr Ala Asn Val Phe Glu	
40 45 50	
cgg gtt ccg ttc ctg aac tac ttc cgc aac tcg atc atc atc acg gtt	307
Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser Ile Ile Ile Thr Val	
55 60 65	
att ttg tgt ctg gtg aag att atc ttg ggt gtg atc tct gca tat gcg	355
Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val Ile Ser Ala Tyr Ala	
70 75 80 85	
ttg tcg att ttg cgc ttc ccg ggt cga aac ctt gtg ttc ttg ctg gtt	403
Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu Val Phe Leu Leu Val	
90 95 100	
atc tcc gcg ctg atg gtg cct tcc gaa gtg act gtt att tcc aac tat	451
Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr Val Ile Ser Asn Tyr	
105 110 115	
gcg ttg gtc agt cag ctt ggt tgg cgc gat acc tac cag ggc atc atc	499
Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr Tyr Gln Gly Ile Ile	
120 125 130	
gtt ccg cta gcg ggt att gct ttc gga acg ttc ctc atg cgt aac cac	547
Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe Leu Met Arg Asn His	
135 140 145	
ttc atg tct att cct tct gag ctc att gaa gct gcg cga atg gat cac	595
Phe Met Ser Ile Pro Ser Glu Leu Ile Glu Ala Ala Arg Met Asp His	
150 155 160 165	
tgt gga cac ttc agg ttg ctc tgg aag gtt ttg ctt cca atc tct atg	643
Cys Gly His Phe Arg Leu Leu Trp Lys Val Leu Leu Pro Ile Ser Met	
170 175 180	
cct acg ttg gtg gcg ttc tcc atg atc acc gtg gtg aat gaa tgg aac	691
Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val Val Asn Glu Trp Asn	
185 190 195	
caa tac ctg tgg cct ttc ctg atg gca gaa acc gat aat tca gca act	739
Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr Asp Asn Ser Ala Thr	
200 205 210	
ctg ccc att ggt ttg acc atg ctt caa aac aat gag ggt gtc tcc aac	787
Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn Glu Gly Val Ser Asn	
215 220 225	
tgg gga cct gtc atg gcc gca acg atc atg acc atg ttg cct gtg ctt	835
Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr Met Leu Pro Val Leu	
230 235 240 245	
gtg atg ttc ttg gca ctg cag gag tac atg atc aag gga ctt atc tcc	883
Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile Lys Gly Leu Ile Ser	
250 255 260	

ggc gcc gtc aag ggc taaaaacttc tcgctaaaaa ott
 Gly Ala Val Lys Gly
 265

921

<210> 340

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Gly Tyr Val Gly Met Val Leu Ala Ile Leu Phe Ile Gly Leu Pro
 1 5 10 15

Leu Val Phe Ile Val Leu Thr Ser Phe Lys Gln Gln Ser Glu Ile Tyr
 20 25 30

Thr Gln Pro Val Thr Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr
 35 40 45

Ala Asn Val Phe Glu Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser
 50 55 60

Ile Ile Ile Thr Val Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val
 65 70 75 80

Ile Ser Ala Tyr Ala Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu
 85 90 95

Val Phe Leu Leu Val Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr
 100 105 110

Val Ile Ser Asn Tyr Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr
 115 120 125

Tyr Gln Gly Ile Ile Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe
 130 135 140

Leu Met Arg Asn His Phe Met Ser Ile Pro Ser Glu Leu Ile Glu Ala
 145 150 155 160

Ala Arg Met Asp His Cys Gly His Phe Arg Leu Leu Trp Lys Val Leu
 165 170 175

Leu Pro Ile Ser Met Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val
 180 185 190

Val Asn Glu Trp Asn Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr
 195 200 205

Asp Asn Ser Ala Thr Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn
 210 215 220

Glu Gly Val Ser Asn Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr
 225 230 235 240

Met Leu Pro Val Leu Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile
 245 250 255

Lys Gly Leu Ile Ser Gly Ala Val Lys Gly
 260 265

<210> 341
 <211> 899
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(876)
 <223> RXS00088

<400> 341

atc gaa gac aac cac ggc acc gaa ggg atc tcc ctg cca atc gag ggc	48
Ile Glu Asp Asn His Gly Thr Glu Gly Ile Ser Leu Pro Ile Glu Gly	
1 5 10 15	
gtc gct gcg acc gac aac cgc gca ttc gaa ctg ctt gat cgc tgg ggt	96
Val Ala Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly	
20 25 30	
gta gag ctc gtt gca gct cca ctt cag ctg gtt cca ttt acc gtt acg	144
Val Glu Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr	
35 40 45	
ggc tac acc gaa gag ggc ggc gtc gct aac ctt ggc tcc cac cgc gag	192
Gly Tyr Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu	
50 55 60	
cca gac ctg gaa gca ctt gct gct gca cag cct tcc ctg atc atc aac	240
Pro Asp Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn	
65 70 75 80	
ggc cag cgc ttc gct cag tac tac gat gac atc att gcc ctg aac cct	288
Gly Gln Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro	
85 90 95	
gac gca acc gtt gtt gag cta gac cca cgc gat ggc gag cca ctt gac	336
Asp Ala Thr Val Val Glu Leu Asp Pro Arg Asp Gly Glu Pro Leu Asp	
100 105 110	
cag gag ctt atc cgc cag gct gaa acc ctc ggt gag atc ttc ggc gaa	384
Gln Glu Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu	
115 120 125	
gaa gaa gat gct gca aag atc gtt gct gat ttc gag tcc gca ctt gag	432
Glu Glu Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu	
130 135 140	
cgc gct aag acc gca tac gca gca atc tcc gac cag acc gtc atg gca	480
Arg Ala Lys Thr Ala Tyr Ala Ala Ile Ser Asp Gln Thr Val Met Ala	
145 150 155 160	
gtt aac gtt tcc ggc gga aac att ggc tac atc gct cct tcc gtt gga	528
Val Asn Val Ser Gly Gly Asn Ile Gly Tyr Ile Ala Pro Ser Val Gly	
165 170 175	
cgc acc tac ggt cca atc ttc gac ctg gtt gga ctc acc cca gca ctc	576
Arg Thr Tyr Gly Pro Ile Phe Asp Leu Val Gly Leu Thr Pro Ala Leu	
180 185 190	

gag gtt ggc aac gcg tcc tcc gac cac gag ggc gac gac att aac gtc 624
 Glu Val Gly Asn Ala Ser Ser Asp His Glu Gly Asp Asp Ile Asn Val
 195 200 205

gaa gca atc gca gct gca aac cca gac ctg atc ctg gtc atg gac cgc 672
 Glu Ala Ile Ala Ala Ala Asn Pro Asp Leu Ile Leu Val Met Asp Arg
 210 215 220

gat ggt ggc acc agc acc cgc aac gaa gct gat tac gtt cca gca gag 720
 Asp Gly Gly Thr Ser Thr Arg Asn Glu Ala Asp Tyr Val Pro Ala Glu
 225 230 235 240

cag atc gtc tcc gac aat gaa gca ctg gca aac gtc aag gct gtc acc 768
 Gln Ile Val Ser Asp Asn Glu Ala Leu Ala Asn Val Lys Ala Val Thr
 245 250 255

gac gga tac gtt tac tac gca cct gca gat acc tac acc aac gaa aac 816
 Asp Gly Tyr Val Tyr Tyr Ala Pro Ala Asp Thr Tyr Thr Asn Glu Asn
 260 265 270

atc atc acc tac acc gag atc ctc aac ggc atg gca gat atg ttc gag 864
 Ile Ile Thr Tyr Thr Glu Ile Leu Asn Gly Met Ala Asp Met Phe Glu
 275 280 285

aag gca gct cag taggggatcg atccacact gac 899
 Lys Ala Ala Gln
 290

<210> 342
 <211> 292
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 342
 Ile Glu Asp Asn His Gly Thr Glu Gly Ile Ser Leu Pro Ile Glu Gly
 1 5 10 15

Val Ala Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly
 20 25 30

Val Glu Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr
 35 40 45

Gly Tyr Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu
 50 55 60

Pro Asp Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn
 65 70 75 80

Gly Gln Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro
 85 90 95

Asp Ala Thr Val Val Glu Leu Asp Pro Arg Asp Gly Glu Pro Leu Asp
 100 105 110

Gln Glu Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu
 115 120 125

Glu Glu Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu
 130 135 140

Arg Ala Lys Thr Ala Tyr Ala Ala Ile Ser Asp Gln Thr Val Met Ala
 145 150 155 160
 Val Asn Val Ser Gly Gly Asn Ile Gly Tyr Ile Ala Pro Ser Val Gly
 165 170 175
 Arg Thr Tyr Gly Pro Ile Phe Asp Leu Val Gly Leu Thr Pro Ala Leu
 180 185 190
 Glu Val Gly Asn Ala Ser Ser Asp His Glu Gly Asp Asp Ile Asn Val
 195 200 205
 Glu Ala Ile Ala Ala Ala Asn Pro Asp Leu Ile Leu Val Met Asp Arg
 210 215 220
 Asp Gly Gly Thr Ser Thr Arg Asn Glu Ala Asp Tyr Val Pro Ala Glu
 225 230 235 240
 Gln Ile Val Ser Asp Asn Glu Ala Leu Ala Asn Val Lys Ala Val Thr
 245 250 255
 Asp Gly Tyr Val Tyr Tyr Ala Pro Ala Asp Thr Tyr Thr Asn Glu Asn
 260 265 270
 Ile Ile Thr Tyr Thr Glu Ile Leu Asn Gly Met Ala Asp Met Phe Glu
 275 280 285
 Lys Ala Ala Gln
 290

<210> 343
 <211> 1200
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1177)
 <223> RXS00372

<400> 343
 gcagacat ttt ccataagtcc tgcgaaatgc gccattcat gtaaagatgt tatttcctcc 60
 cccaaacact ccttaaaatt tcaagaagg ccttattttc atg tct tcg aag cac 115
 Met Ser Ser Lys His
 1 5
 cct ttg aag cgc act gcc gtt act gtt ttt gca ctc ggc gct tcc gct 163
 Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala Leu Gly Ala Ser Ala
 10 15 20
 gct ctc ctc gtg gct tgc tct gaa cct tct gag gac gtt tcc acc gca 211
 Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu Asp Val Ser Thr Ala
 25 30 35
 gag acc acc act gca agc tct tcc gct aac gca tcc gat gca gcc ggt 259
 Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala Ser Asp Ala Ala Gly
 40 45 50

gaa aaa gta acc atc acc gtc tac acc tct gag cct gag gaa aag gtc 307
 Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu Pro Glu Glu Lys Val
 55 60 65

gat gag atc aac aag gcg ttc atg gaa gcc aac cca gat att gag gtt 355
 Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn Pro Asp Ile Glu Val
 70 75 80 85

gag gtg tac cgc gct ggt act ggc gat ctg act gct cgc att gaa gct 403
 Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr Ala Arg Ile Glu Ala
 90 95 100

gaa aag gca tcc ggt tct atc gag gct gat gtg ttg tgg gct gcg gat 451
 Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val Leu Trp Ala Ala Asp
 105 110 115

gct gca acc ttt gaa act tat gca gca cag ggc gac ctt gca gag ctg 499
 Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly Asp Leu Ala Glu Leu
 120 125 130

gaa gat gtt gag act tcc gac atc att gaa gag gct ctg gat gct gag 547
 Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu Ala Leu Asp Ala Glu
 135 140 145

aac ttt tat gta ggc acc cgc atc atc cca acc gtg att gca tac aac 595
 Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr Val Ile Ala Tyr Asn
 150 155 160 165

act gaa gtt gtt gat cag gct gag ctt cct acg tct tgg gct gat ctg 643
 Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr Ser Trp Ala Asp Leu
 170 175 180

act gat cct aag tat gca ggc caa ctg gtc atg ccg gat cca gct gtg 691
 Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met Pro Asp Pro Ala Val
 185 190 195

tct ggt gct gca gcc ttc aat gct tct gtg tgg aag aac gac cct gcg 739
 Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp Lys Asn Asp Pro Ala
 200 205 210

ctt ggc gaa gcc tgg atc acc gcc ttg ggt gaa aac caa cca atg atc 787
 Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu Asn Gln Pro Met Ile
 215 220 225

gct cag tcc aac ggc cca acc tcc cag gag atc gct ggc ggt ggc cac 835
 Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile Ala Gly Gly Gly His
 230 235 240 245

cca gtg ggc atc gtg gtg gac tac ttg gtg cgc gac ttg gct gct gct 883
 Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg Asp Leu Ala Ala Ala
 250 255 260

gga tct cca atc gac acc atc tac gca tcg gag ggt tct cct tac atc 931
 Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu Gly Ser Pro Tyr Ile
 265 270 275

act gag cct gca ggt gtg ttc gct gat tct gaa aag aag gaa gca gcc 979
 Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu Lys Lys Glu Ala Ala
 280 285 290

gag cgc tac atc aac ttc ctg ctg tct gtt gaa ggc cag gaa atc gca 1027

00606664 00606664

Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu Gly Gln Glu Ile Ala
 295 300 305
 gtt gag cag gca tac ctg cca gtg cgt gaa gat gtc gga act cca gag 1075
 Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp Val Gly Thr Pro Glu
 310 315 320 325
 ggc acc ccc gag ttg gct gac atc gag ctc atg acc cct gac ctg gag 1123
 Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met Thr Pro Asp Leu Glu
 330 335 340
 gtt gta acc gct gat aag gcg gct gct gtt gag ttc ttc caa aac gca 1171
 Val Val Thr Ala Asp Lys Ala Ala Ala Val Glu Phe Phe Gln Asn Ala
 345 350 355
 atg aac tagttttcct atgcagttat ctc 1200
 Met Asn

<210> 344

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ser Ser Lys His Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala
 1 5 10 15
 Leu Gly Ala Ser Ala Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu
 20 25 30
 Asp Val Ser Thr Ala Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala
 35 40 45
 Ser Asp Ala Ala Gly Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu
 50 55 60
 Pro Glu Glu Lys Val Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn
 65 70 75 80
 Pro Asp Ile Glu Val Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr
 85 90 95
 Ala Arg Ile Glu Ala Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val
 100 105 110
 Leu Trp Ala Ala Asp Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly
 115 120 125
 Asp Leu Ala Glu Leu Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu
 130 135 140
 Ala Leu Asp Ala Glu Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr
 145 150 155 160
 Val Ile Ala Tyr Asn Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr
 165 170 175
 Ser Trp Ala Asp Leu Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met
 180 185 190

Pro Asp Pro Ala Val Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp
 195 200 205

Lys Asn Asp Pro Ala Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu
 210 215 220

Asn Gln Pro Met Ile Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile
 225 230 235 240

Ala Gly Gly Gly His Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg
 245 250 255

Asp Leu Ala Ala Ala Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu
 260 265 270

Gly Ser Pro Tyr Ile Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu
 275 280 285

Lys Lys Glu Ala Ala Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu
 290 295 300

Gly Gln Glu Ile Ala Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp
 305 310 315 320

Val Gly Thr Pro Glu Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met
 325 330 335

Thr Pro Asp Leu Glu Val Val Thr Ala Asp Lys Ala Ala Ala Val Glu
 340 345 350

Phe Phe Gln Asn Ala Met Asn
 355

<210> 345
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXS02590

<400> 345
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ggtcttacct ccacctggcc cctcgtgggc tggttccctc atg ggc atc tca ttg 115
 Met Gly Ile Ser Leu
 1 5

ttg tca tca ctg ttg aaa atc cat ggt ttt cca gtc gtc gca gat ttc 163
 Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro Val Val Ala Asp Phe
 10 15 20

ttc ttc gcg tta gct gtt gtg gtg gca att gtc att att ggc ggt tgg 211
 Phe Phe Ala Leu Ala Val Val Val Ala Ile Val Ile Ile Gly Gly Trp
 25 30 35

cta atc tac cgc tct cct tca ttc aaa act gaa gtc atg ccg gca tgg 259

Leu	Ile	Tyr	Arg	Ser	Pro	Ser	Phe	Lys	Thr	Glu	Val	Met	Pro	Ala	Trp		
	40						45					50					
gca	atg	ctg	tcc	atg	ggg	ttg	atc	gca	ttg	gga	act	gca	agc	ccc	gta	307	
Ala	Met	Leu	Ser	Met	Gly	Leu	Ile	Ala	Leu	Gly	Thr	Ala	Ser	Pro	Val		
	55					60				65							
gtt	ttg	ggg	gat	gat	ctg	tgg	gga	ttt	atg	ttt	gtg	tgc	tgg	tct	att	355	
Val	Leu	Gly	Asp	Asp	Leu	Trp	Gly	Phe	Met	Phe	Val	Cys	Trp	Ser	Ile		
	70				75					80					85		
ggc	aca	gcc	gtg	gga	ctt	gtt	gcc	tat	tcc	tta	tat	ata	acg	gcc	att	403	
Gly	Thr	Ala	Val	Gly	Leu	Val	Ala	Tyr	Ser	Leu	Tyr	Ile	Thr	Ala	Ile		
				90				95						100			
ttg	cga	tct	aag	gcg	ggc	aca	cca	act	ttt	gcg	tgg	ggg	ctt	cct	ctt	451	
Leu	Arg	Ser	Lys	Ala	Gly	Thr	Pro	Thr	Phe	Ala	Trp	Gly	Leu	Pro	Leu		
			105					110					115				
gtc	acg	ccg	atg	gtt	gct	tcc	acc	tgc	gca	gca	caa	ctc	cat	gag	cac	499	
Val	Thr	Pro	Met	Val	Ala	Ser	Thr	Ser	Ala	Ala	Gln	Leu	His	Glu	His		
			120				125					130					
ttt	gaa	ctt	ccg	gcg	atg	ctg	tgg	gtt	tct	ttc	ggg	ctc	ttc	ctt	tta	547	
Phe	Glu	Leu	Pro	Ala	Met	Leu	Trp	Val	Ser	Phe	Gly	Leu	Phe	Leu	Leu		
	135					140					145						
act	ttg	gcg	tct	gca	cca	gca	gtt	ttt	acc	cga	gtg	tat	ttc	tac	tat	595	
Thr	Leu	Ala	Ser	Ala	Pro	Ala	Val	Phe	Thr	Arg	Val	Tyr	Phe	Tyr	Tyr		
	150				155				160						165		
ttc	ggc	ccc	aag	gcg	cag	ggc	atc	cca	ctg	atg	gca	aca	cca	aca	tca	643	
Phe	Gly	Pro	Lys	Ala	Gln	Gly	Ile	Pro	Leu	Met	Ala	Thr	Pro	Thr	Ser		
				170				175						180			
tgg	att	cct	ttg	ggg	atg	gtg	ggc	caa	tcc	act	gca	gca	gct	cag	ctc	691	
Trp	Ile	Pro	Leu	Gly	Met	Val	Gly	Gln	Ser	Thr	Ala	Ala	Ala	Gln	Leu		
			185				190						195				
atc	ggg	gcg	tcc	ttt	gga	tcc	aag	aca	gca	atc	aca	atg	ggc	att	att	739	
Ile	Gly	Ala	Ser	Phe	Gly	Ser	Lys	Thr	Ala	Ile	Thr	Met	Gly	Ile	Ile		
		200					205					210					
tac	ggc	atc	atc	atg	gga	att	ttt	acg	att	cct	ctg	gga	gcc	atc	gct	787	
Tyr	Gly	Ile	Ile	Met	Gly	Ile	Phe	Thr	Ile	Pro	Leu	Gly	Ala	Ile	Ala		
	215					220					225						
cac	ttt	gtg	ttc	tac	aga	gct	gtt	ttc	aaa	ggg	gcg	aca	tac	agc	ccc	835	
His	Phe	Val	Phe	Tyr	Arg	Ala	Val	Phe	Lys	Gly	Ala	Thr	Tyr	Ser	Pro		
	230				235				240						245		
aca	tgg	tgg	gcc	agt	acc	ttc	cca	gtt	ggc	act	ttg	agt	ttg	ggg	gcg	883	
Thr	Trp	Trp	Ala	Ser	Thr	Phe	Pro	Val	Gly	Thr	Leu	Ser	Leu	Gly	Ala		
			250					255						260			
cat	ttt	tta	tca	cag	agc	acc	gga	gtg	gag	tgg	ttt	aac	tac	ttc	agc	931	
His	Phe	Leu	Ser	Gln	Ser	Thr	Gly	Val	Glu	Trp	Phe	Asn	Tyr	Phe	Ser		
		265					270					275					
ctg	tac	ttg	att	gct	tta	atg	ctc	ttt	cat	gtc	atc	gtg	tcc	acc	atc	979	
Leu	Tyr	Leu	Ile	Ala	Leu	Met	Leu	Phe	His	Val	Ile	Val	Ser	Thr	Ile		

280 285 290
 gcc ggt acg att gca gta atg aga aga atc gtc gga aag ctt aaa tct 1027
 Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val Gly Lys Leu Lys Ser
 295 300 305

 caa ctg gcc taaattgcag cgagaggtct aaa 1059
 Gln Leu Ala
 310

 <210> 346
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 346
 Met Gly Ile Ser Leu Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro
 1 5 10 15
 Val Val Ala Asp Phe Phe Phe Ala Leu Ala Val Val Val Ala Ile Val
 20 25 30
 Ile Ile Gly Gly Trp Leu Ile Tyr Arg Ser Pro Ser Phe Lys Thr Glu
 35 40 45
 Val Met Pro Ala Trp Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly
 50 55 60
 Thr Ala Ser Pro Val Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe
 65 70 75 80
 Val Cys Trp Ser Ile Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu
 85 90 95
 Tyr Ile Thr Ala Ile Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala
 100 105 110
 Trp Gly Leu Pro Leu Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala
 115 120 125
 Gln Leu His Glu His Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe
 130 135 140
 Gly Leu Phe Leu Leu Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg
 145 150 155 160
 Val Tyr Phe Tyr Tyr Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met
 165 170 175
 Ala Thr Pro Thr Ser Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr
 180 185 190
 Ala Ala Ala Gln Leu Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile
 195 200 205
 Thr Met Gly Ile Ile Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro
 210 215 220
 Leu Gly Ala Ile Ala His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly
 225 230 235 240

Ala Thr Tyr Ser Pro Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr
 245 250 255

Leu Ser Leu Gly Ala His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp
 260 265 270

Phe Asn Tyr Phe Ser Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val
 275 280 285

Ile Val Ser Thr Ile Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val
 290 295 300

Gly Lys Leu Lys Ser Gln Leu Ala
 305 310

<210> 347

<211> 1725

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1702)

<223> RXS00758

<400> 347

ttcaagtttg gctgtgactc atgtcgcaca tagtatttca atcacgggat ccgcacgatt 60

gcaaaatcct ggggaatatt cataacaacg gaggtcactc atg act ttg aag aag 115
 Met Thr Leu Lys Lys
 1 5

tct ctc gct gta acc acg gcg gct gca ctt gct ttg agc ctt gcc gct 163
 Ser Leu Ala Val Thr Thr Ala Ala Ala Leu Ala Leu Ser Leu Ala Ala
 10 15 20

tgc tcg tcc gac tcc tcg tcc gac agc tcc tca tcc tca tca ggc agc 211
 Cys Ser Ser Asp Ser Ser Ser Asp Ser Ser Ser Ser Ser Gly Ser
 25 30 35

gaa ggc ggc gac aac tac gtc ctc gtc aac ggc act gag cca cag aac 259
 Glu Gly Gly Asp Asn Tyr Val Leu Val Asn Gly Thr Glu Pro Gln Asn
 40 45 50

ccg ctc gtc cca ggc aac acc aac gaa gta ggt ggc ggt cgc atc gtc 307
 Pro Leu Val Pro Gly Asn Thr Asn Glu Val Gly Gly Gly Arg Ile Val
 55 60 65

gac agc atc ttc tcc ggc ctg gtc tac tac gac gtc gac ggc tcc cct 355
 Asp Ser Ile Phe Ser Gly Leu Val Tyr Tyr Asp Val Asp Gly Ser Pro
 70 75 80 85

gtc aac gat gtt gca gag tcc atc gaa ctc gaa ggt gac aag acc tac 403
 Val Asn Asp Val Ala Glu Ser Ile Glu Leu Glu Gly Asp Lys Thr Tyr
 90 95 100

cgc atc acc atc aaa gac ggc cag acc ttc acc gat ggc acc cca gtt 451
 Arg Ile Thr Ile Lys Asp Gly Gln Thr Phe Thr Asp Gly Thr Pro Val
 105 110 115

acc gct gag agc ttt gtc aac gca tgg aac tac aac gta gct aac agc 499
 Thr Ala Glu Ser Phe Val Asn Ala Trp Asn Tyr Asn Val Ala Asn Ser
 120 125 130

acg ctg tcc tcc tac ttc ttt gag tcc atc ctc ggc tac gaa gaa ggc 547
 Thr Leu Ser Ser Tyr Phe Phe Glu Ser Ile Leu Gly Tyr Glu Glu Gly
 135 140 145

gtc gag tcc atg gaa ggc ctc cag gtc gtc gac gac acc acc ttc acc 595
 Val Glu Ser Met Glu Gly Leu Gln Val Val Asp Asp Thr Thr Phe Thr
 150 155 160 165

gtc gag ctc acc cag cct gag tcc gac ttc cca ctg cgc ctg gga tac 643
 Val Glu Leu Thr Gln Pro Glu Ser Asp Phe Pro Leu Arg Leu Gly Tyr
 170 175 180

tcc gca ttc ttc ccg ctt cct gaa tcc gca ttt gac gac atg gac gca 691
 Ser Ala Phe Phe Pro Leu Pro Glu Ser Ala Phe Asp Asp Met Asp Ala
 185 190 195

ttc ggt gag aac cca atc ggc aac ggt cca tac aag ctc caa gag tgg 739
 Phe Gly Glu Asn Pro Ile Gly Asn Gly Pro Tyr Lys Leu Gln Glu Trp
 200 205 210

aac cac aac cag gac gcc acc atc gtt cct aac gcg gac tac acc ggt 787
 Asn His Asn Gln Asp Ala Thr Ile Val Pro Asn Ala Asp Tyr Thr Gly
 215 220 225

gga cgc cag gct cag aac gac ggc gtg aag ttc atc ttc tac cca acc 835
 Gly Arg Gln Ala Gln Asn Asp Gly Val Lys Phe Ile Phe Tyr Pro Thr
 230 235 240 245

ttc gac tcc gct tac gcg gac ctg ctc tcc gac aac ttg gat gtg ctg 883
 Phe Asp Ser Ala Tyr Ala Asp Leu Leu Ser Asp Asn Leu Asp Val Leu
 250 255 260

gac gct atc cca gac tcc gcg ttc tcc tcc ttc gag gac gag ctc tct 931
 Asp Ala Ile Pro Asp Ser Ala Phe Ser Ser Phe Glu Asp Glu Leu Ser
 265 270 275

ggc cgt tcc atc aac cag cct tcc gct gtg ttc cag tcc ttc acc atc 979
 Gly Arg Ser Ile Asn Gln Pro Ser Ala Val Phe Gln Ser Phe Thr Ile
 280 285 290

ccg gag agc ctt gag cac ttc tcc ggc gaa gaa ggc gtg ctg cgt cgc 1027
 Pro Glu Ser Leu Glu His Phe Ser Gly Glu Glu Gly Val Leu Arg Arg
 295 300 305

cag gcc atc tcc ttg gcc gtc aac cgc gac gag atc acc caa acc atc 1075
 Gln Ala Ile Ser Leu Ala Val Asn Arg Asp Glu Ile Thr Gln Thr Ile
 310 315 320 325

ttc gaa ggc acc cgc acc cca gcg acg gac ttc acc tcc cct gtc atc 1123
 Phe Glu Gly Thr Arg Thr Pro Ala Thr Asp Phe Thr Ser Pro Val Ile
 330 335 340

gac gga cac tct gat tcc ctc cag ggc gca gat gtc ttg acc tac gat 1171
 Asp Gly His Ser Asp Ser Leu Gln Gly Ala Asp Val Leu Thr Tyr Asp
 345 350 355

cca gag cgc gct cag gaa ctg tgg gca cag gca gac gag atc agc cct 1219
 Pro Glu Arg Ala Gln Glu Leu Trp Ala Gln Ala Asp Glu Ile Ser Pro
 360 365 370

tgg tcc ggc gag ttc tcc atc tcc tac aac gca gac ggt gga cac cag 1267
 Trp Ser Gly Glu Phe Ser Ile Ser Tyr Asn Ala Asp Gly Gly His Gln
 375 380 385

gca tgg gtg gac gca acc gcc aat tcc atc cgc aac acc ctg ggt atc 1315
 Ala Trp Val Asp Ala Thr Ala Asn Ser Ile Arg Asn Thr Leu Gly Ile
 390 395 400 405

gac gcc atc ggc aac cca tac cca gac ttc aag tcc ctg cgt gac gat 1363
 Asp Ala Ile Gly Asn Pro Tyr Pro Asp Phe Lys Ser Leu Arg Asp Asp
 410 415 420

gtc acc aac cgc acc atc aac ggc gca ttc cgc acc ggc tgg cag gca 1411
 Val Thr Asn Arg Thr Ile Asn Gly Ala Phe Arg Thr Gly Trp Gln Ala
 425 430 435

gac tac ccg tcc ttg ggc aac ttc ctc gga cct ttg tac ggc acc ggt 1459
 Asp Tyr Pro Ser Leu Gly Asn Phe Leu Gly Pro Leu Tyr Gly Thr Gly
 440 445 450

gca ggc tcc aac gat ggt gac tac tcc aac cca gat ttc gat gcc aag 1507
 Ala Gly Ser Asn Asp Gly Asp Tyr Ser Asn Pro Asp Phe Asp Ala Lys
 455 460 465

ctc gcc gaa gca gca aac gcg gcc gat gtt gac gca tca acc ccg cta 1555
 Leu Ala Glu Ala Ala Asn Ala Ala Asp Val Asp Ala Ser Thr Pro Leu
 470 475 480 485

tac aac gaa gca cag gaa atc ctg ctc cag gat ctc cca gcg atc cca 1603
 Tyr Asn Glu Ala Gln Glu Ile Leu Leu Gln Asp Leu Pro Ala Ile Pro
 490 495 500

act tgg tac tcc aac gca gtt ggt gga tac tcc acc aac gtg gac aac 1651
 Thr Trp Tyr Ser Asn Ala Val Gly Gly Tyr Ser Thr Asn Val Asp Asn
 505 510 515

gtg gaa ttc cag tgg aac tcg caa cct gcg tac tac cag atc acc aag 1699
 Val Glu Phe Gln Trp Asn Ser Gln Pro Ala Tyr Tyr Gln Ile Thr Lys
 520 525 530

aac tagtagcttc gcaccacccg ctc 1725
 Asn

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<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

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Ser Ser Ser Gly Ser Glu Gly Gly Asp Asn Tyr Val Leu Val Asn Gly
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 Thr Glu Pro Gln Asn Pro Leu Val Pro Gly Asn Thr Asn Glu Val Gly
 50 55 60
 Gly Gly Arg Ile Val Asp Ser Ile Phe Ser Gly Leu Val Tyr Tyr Asp
 65 70 75 80
 Val Asp Gly Ser Pro Val Asn Asp Val Ala Glu Ser Ile Glu Leu Glu
 85 90 95
 Gly Asp Lys Thr Tyr Arg Ile Thr Ile Lys Asp Gly Gln Thr Phe Thr
 100 105 110
 Asp Gly Thr Pro Val Thr Ala Glu Ser Phe Val Asn Ala Trp Asn Tyr
 115 120 125
 Asn Val Ala Asn Ser Thr Leu Ser Ser Tyr Phe Phe Glu Ser Ile Leu
 130 135 140
 Gly Tyr Glu Glu Gly Val Glu Ser Met Glu Gly Leu Gln Val Val Asp
 145 150 155 160
 Asp Thr Thr Phe Thr Val Glu Leu Thr Gln Pro Glu Ser Asp Phe Pro
 165 170 175
 Leu Arg Leu Gly Tyr Ser Ala Phe Phe Pro Leu Pro Glu Ser Ala Phe
 180 185 190
 Asp Asp Met Asp Ala Phe Gly Glu Asn Pro Ile Gly Asn Gly Pro Tyr
 195 200 205
 Lys Leu Gln Glu Trp Asn His Asn Gln Asp Ala Thr Ile Val Pro Asn
 210 215 220
 Ala Asp Tyr Thr Gly Gly Arg Gln Ala Gln Asn Asp Gly Val Lys Phe
 225 230 235 240
 Ile Phe Tyr Pro Thr Phe Asp Ser Ala Tyr Ala Asp Leu Leu Ser Asp
 245 250 255
 Asn Leu Asp Val Leu Asp Ala Ile Pro Asp Ser Ala Phe Ser Ser Phe
 260 265 270
 Glu Asp Glu Leu Ser Gly Arg Ser Ile Asn Gln Pro Ser Ala Val Phe
 275 280 285
 Gln Ser Phe Thr Ile Pro Glu Ser Leu Glu His Phe Ser Gly Glu Glu
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 Gly Val Leu Arg Arg Gln Ala Ile Ser Leu Ala Val Asn Arg Asp Glu
 305 310 315 320
 Ile Thr Gln Thr Ile Phe Glu Gly Thr Arg Thr Pro Ala Thr Asp Phe
 325 330 335
 Thr Ser Pro Val Ile Asp Gly His Ser Asp Ser Leu Gln Gly Ala Asp
 340 345 350
 Val Leu Thr Tyr Asp Pro Glu Arg Ala Gln Glu Leu Trp Ala Gln Ala

355	360	365
Asp Glu Ile Ser Pro Trp Ser Gly Glu Phe Ser Ile Ser Tyr Asn Ala 370 375 380		
Asp Gly Gly His Gln Ala Trp Val Asp Ala Thr Ala Asn Ser Ile Arg 385 390 395 400		
Asn Thr Leu Gly Ile Asp Ala Ile Gly Asn Pro Tyr Pro Asp Phe Lys 405 410 415		
Ser Leu Arg Asp Asp Val Thr Asn Arg Thr Ile Asn Gly Ala Phe Arg 420 425 430		
Thr Gly Trp Gln Ala Asp Tyr Pro Ser Leu Gly Asn Phe Leu Gly Pro 435 440 445		
Leu Tyr Gly Thr Gly Ala Gly Ser Asn Asp Gly Asp Tyr Ser Asn Pro 450 455 460		
Asp Phe Asp Ala Lys Leu Ala Glu Ala Ala Asn Ala Ala Asp Val Asp 465 470 475 480		
Ala Ser Thr Pro Leu Tyr Asn Glu Ala Gln Glu Ile Leu Leu Gln Asp 485 490 495		
Leu Pro Ala Ile Pro Thr Trp Tyr Ser Asn Ala Val Gly Gly Tyr Ser 500 505 510		
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Tyr Gln Ile Thr Lys Asn 530		
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Met Arg Thr Ala Thr 1 5		
aaa gtc atc gca aca gtg atg gcc tca acc ctg gct atc ggg ctg gca 163		
Lys Val Ile Ala Thr Val Met Ala Ser Thr Leu Ala Ile Gly Leu Ala 10 15 20		
tct tgt tcc agc tct agt ggc acc cca gac gtg aat tac gta tcc gtc 211		
Ser Cys Ser Ser Ser Ser Gly Thr Pro Asp Val Asn Tyr Val Ser Val 25 30 35		

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 Asn Gly Thr Glu Pro Gln Arg Gly Leu Ile Pro Gly Asp Thr Asn Glu
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aac ggc ggt ggg cga gtg gtg gac atg ctg tac tct ggg ctc gtc tac 307
 Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr Ser Gly Leu Val Tyr
 55 60 65

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 Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu Ala Ala Ser Ile Asp
 70 75 80 85

cag gaa aca gac acc acc tac aaa atc act ttg cgt gat ggc atc aaa 403
 Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu Arg Asp Gly Ile Lys
 90 95 100

ttc agt gac gga tcg gat att act gcc act gat ttt gtg gat acc tgg 451
 Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp Phe Val Asp Thr Trp
 105 110 115

aat ttt gta gtg gaa aat gga ctg ctc aac act tct ttc ttc tca ccg 499
 Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr Ser Phe Phe Ser Pro
 120 125 130

att aaa ggg tat gag gag ggc gtg gaa acg ctc gag ggt ttg aat gtg 547
 Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu Glu Gly Leu Asn Val
 135 140 145

gtg gat gat cgc aca ttt acc atc gag ctt gcc caa ccg gat tct gag 595
 Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala Gln Pro Asp Ser Glu
 150 155 160 165

ttc acc caa cgc att ggc tac tac ggt ttt gca ccg atg cca gct tcg 643
 Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala Pro Met Pro Ala Ser
 170 175 180

gct cgc gat gat att gac gcc ttt ggt gaa aac ccc gtg tcc tct ggc 691
 Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn Pro Val Ser Ser Gly
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cct tac aaa cta gag cag tgg gat cac aac gca gaa ctg aaa gtg gtg 739
 Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala Glu Leu Lys Val Val
 200 205 210

gcc aat gaa cac tac gat ggc ccg cgc gca gcc aac aac gat ggc ttg 787
 Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala Asn Asn Asp Gly Leu
 215 220 225

aag tac gtg ttc tac gcc caa aat gat gca gct tat tca gat ctg ttg 835
 Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala Tyr Ser Asp Leu Leu
 230 235 240 245

gct gga aac cta gat gtg ctg gat ctc att cca cca tcg gcg tac acc 883
 Ala Gly Asn Leu Asp Val Leu Asp Leu Ile Pro Pro Ser Ala Tyr Thr
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acc tat gaa gag gaa ctg tcg ggt cga tcc att aat caa cct gcg gcc 931
 Thr Tyr Glu Glu Glu Leu Ser Gly Arg Ser Ile Asn Gln Pro Ala Ala
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tcc tat ctg gaa ctc tcc att cgc atg gaa tcc ccc aac ttt gaa ggg 979

Ser	Tyr	Leu	Glu	Leu	Ser	Ile	Arg	Met	Glu	Ser	Pro	Asn	Phe	Glu	Gly	
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caa	cag	gga	cag	ttg	cgt	cga	caa	gca	att	tct	atg	gcg	att	aac	cgt	1027
Gln	Gln	Gly	Gln	Leu	Arg	Arg	Gln	Ala	Ile	Ser	Met	Ala	Ile	Asn	Arg	
	295					300					305					
gaa	gaa	atc	gct	gag	cag	atc	ttc	gcc	ggc	acc	tac	acg	cct	gcg	ctc	1075
Glu	Glu	Ile	Ala	Glu	Gln	Ile	Phe	Ala	Gly	Thr	Tyr	Thr	Pro	Ala	Leu	
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Asp	Phe	Thr	Ala	Pro	Val	Leu	Asp	Gly	Trp	Arg	Asp	Asp	Leu	Asn	Gly	
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Asn	Asp	Val	Leu	Thr	Phe	Gln	Pro	Asp	Lys	Ala	Arg	Glu	Leu	Trp	Glu	
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Asp	Ala	Glu	Glu	Ile	Ala	Pro	Phe	Glu	Gly	Glu	Leu	Gln	Ile	Ser	Tyr	
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atc	agc	aac	gaa	tta	gac	gtc	aac	gcc	act	ggc	aat	cct	ttc	ccc	gat	1315
Ile	Ser	Asn	Glu	Leu	Asp	Val	Asn	Ala	Thr	Gly	Asn	Pro	Phe	Pro	Asp	
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Phe	Lys	Ser	Phe	Arg	Asp	Thr	Tyr	Arg	Thr	Thr	Gly	Leu	Asp	Gly	Ala	
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tac	cgc	acc	gcg	tgg	ttt	gcg	gac	tac	cca	agc	atc	ggc	aac	ttc	ctt	1411
Tyr	Arg	Thr	Ala	Trp	Phe	Ala	Asp	Tyr	Pro	Ser	Ile	Gly	Asn	Phe	Leu	
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Gly	Pro	Asn	Tyr	Thr	Ser	Gly	Val	Ala	Ser	Asn	Asp	Ala	Lys	Tyr	Glu	
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aac	cca	gaa	ttt	gat	caa	ttg	att	gcc	gac	gcc	gca	gca	gcc	tcc	acc	1507
Asn	Pro	Glu	Phe	Asp	Gln	Leu	Ile	Ala	Asp	Ala	Ala	Ala	Ala	Ser	Thr	
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aag	gag	gaa	acc	ttc	cag	gca	tat	gcg	cag	gcc	cag	gaa	atg	ttg	ttg	1555
Lys	Glu	Glu	Thr	Phe	Gln	Ala	Tyr	Ala	Gln	Ala	Gln	Glu	Met	Leu	Leu	
470					475					480					485	
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525

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<213> *Corynebacterium glutamicum*

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Gly Asp Thr Asn Glu Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr
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Ser Gly Leu Val Tyr Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu
 65 70 75 80

Ala Ala Ser Ile Asp Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu
 85 90 95

Arg Asp Gly Ile Lys Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp
 100 105 110

Phe Val Asp Thr Trp Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr
 115 120 125

Ser Phe Phe Ser Pro Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu
 130 135 140

Glu Gly Leu Asn Val Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala
 145 150 155 160

Gln Pro Asp Ser Glu Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala
 165 170 175

Pro Met Pro Ala Ser Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn
 180 185 190

Pro Val Ser Ser Gly Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala
 195 200 205

Glu Leu Lys Val Val Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala
 210 215 220

Asn Asn Asp Gly Leu Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala
 225 230 235 240

Tyr Ser Asp Leu Leu Ala Gly Asn Leu Asp Val Leu Asp Leu Ile Pro
 245 250 255

Pro Ser Ala Tyr Thr Thr Tyr Glu Glu Glu Leu Ser Gly Arg Ser Ile
 260 265 270

Asn Gln Pro Ala Ala Ser Tyr Leu Glu Leu Ser Ile Arg Met Glu Ser

275 280 285
 Pro Asn Phe Glu Gly Gln Gln Gly Gln Leu Arg Arg Gln Ala Ile Ser
 290 295 300
 Met Ala Ile Asn Arg Glu Glu Ile Ala Glu Gln Ile Phe Ala Gly Thr
 305 310 315 320
 Tyr Thr Pro Ala Leu Asp Phe Thr Ala Pro Val Leu Asp Gly Trp Arg
 325 330 335
 Asp Asp Leu Asn Gly Asn Asp Val Leu Thr Phe Gln Pro Asp Lys Ala
 340 345 350
 Arg Glu Leu Trp Glu Asp Ala Glu Glu Ile Ala Pro Phe Glu Gly Glu
 355 360 365
 Leu Gln Ile Ser Tyr Asn Ala Asp Val Pro Asn Arg Glu Trp Val Asp
 370 375 380
 Ala Val Ala Asn Ser Ile Ser Asn Glu Leu Asp Val Asn Ala Thr Gly
 385 390 395 400
 Asn Pro Phe Pro Asp Phe Lys Ser Phe Arg Asp Thr Tyr Arg Thr Thr
 405 410 415
 Gly Leu Asp Gly Ala Tyr Arg Thr Ala Trp Phe Ala Asp Tyr Pro Ser
 420 425 430
 Ile Gly Asn Phe Leu Gly Pro Asn Tyr Thr Ser Gly Val Ala Ser Asn
 435 440 445
 Asp Ala Lys Tyr Glu Asn Pro Glu Phe Asp Gln Leu Ile Ala Asp Ala
 450 455 460
 Ala Ala Ala Ser Thr Lys Glu Glu Thr Phe Gln Ala Tyr Ala Gln Ala
 465 470 475 480
 Gln Glu Met Leu Leu Arg Asp Leu Pro Ala Ile Pro Leu Trp Tyr Pro
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 Trp Lys Ala Ile Pro Val Tyr Trp Ala Ile Thr Lys Gln
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52

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Asn Ser Ile Asp Arg Leu Leu Gly Leu Asp Gly Thr Val Ser Met Ile
      35          40          45

Gln Cys Ser Met Ala Thr Tyr Ile Cys Trp Thr Leu Asp Thr Thr Val
 50          55          60

Thr Asn Phe Met Met Val Ile Ala Leu Leu Gly Phe Ile Ser Ser Val
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Ser Val Ala Arg Phe Arg Lys Arg Asp Gly Ala
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<223> RXS00453
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<400> 353

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                                   Val Ile Ser Ala Trp
                                   1 5

cta ctt att ttg gcc att gtt ggt ggt ctg gcc ctg acg atg cag aag 163
Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys
                                   10 15 20

ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc 211
Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr Pro Ser Ile Asp Ala
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act gtt tct ctg gtt gaa aat ttc cct gat cag acg aac ccg gtg acg 259
Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln Thr Asn Pro Val Thr
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gcc gcc gga gtt aac gtg gtt ttc caa tcc ccg gaa gga acc acg ctt 307
Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro Glu Gly Thr Thr Leu
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gat gat cct cag atg atg act gcg atg gat gca gtc gtt gat tac att 355
Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala Val Val Asp Tyr Ile
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gag gac aat ttg cct gat ttt ggt ggg gga gag cgc ttc ggc aat cct 403
Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu Arg Phe Gly Asn Pro
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Val Glu Val Ser Pro Ala Leu Glu Glu Met Val Ile Glu Gln Met Thr
                                   105 110 115

agc atg ggg ctt cct gag gaa acc gct gca aag gat gct gcc aat ctg 499
Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys Asp Ala Ala Asn Leu
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gcg gtg ttg agc gaa gac aaa acc att ggc tac acc tct ttc aac att 547
Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr Thr Ser Phe Asn Ile
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gat gtt gag gcc gca gaa tat gtg gag caa aaa cac cgc gat gtg atc 595
Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys His Arg Asp Val Ile
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aac gaa gcg atg caa atc ggt gaa gat tta ggt gtc cgg gtg gaa gcc 643
Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly Val Arg Val Glu Ala
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ggt gga cct gct ttc ggt gat cca att cag att gaa acc acc agt gag 691
Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile Glu Thr Thr Ser Glu
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atc atc ggt att ggc atc gcg ttc atc gtg ttg att ttc acc ttt ggt 739
Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu Ile Phe Thr Phe Gly
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tct ttg att gct gca ggc ttg cct ttg att acc gcg gtg atc ggc gtg 787

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Gly	Ile	Gly	Ala	Leu	Ala	Ile	Val	Leu	Ala	Thr	Ala	Phe	Thr	Asp	Leu	
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Asn	Asn	Val	Thr	Pro	Val	Leu	Ala	Val	Met	Ile	Gly	Leu	Ala	Val	Gly	
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att	gac	tac	gcg	ctg	ttt	att	ttg	tct	agg	tac	cgt	gcg	gag	tat	aag	931
Ile	Asp	Tyr	Ala	Leu	Phe	Ile	Leu	Ser	Arg	Tyr	Arg	Ala	Glu	Tyr	Lys	
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cgc	atg	cca	cgt	gcc	gat	gct	gcc	gga	atg	gcg	gtg	ggc	aca	gct	ggt	979
Arg	Met	Pro	Arg	Ala	Asp	Ala	Ala	Gly	Met	Ala	Val	Gly	Thr	Ala	Gly	
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agt	gcg	gtg	gtg	ttt	gct	ggc	gcg	acg	gtg	att	atc	gcg	ctg	gta	gcc	1027
Ser	Ala	Val	Val	Phe	Ala	Gly	Ala	Thr	Val	Ile	Ile	Ala	Leu	Val	Ala	
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Leu	Ile	Ile	Ala	Asp	Ile	Gly	Phe	Leu	Thr	Ala	Met	Gly	Ile	Ser	Ala	
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Ala	Phe	Thr	Val	Phe	Val	Ala	Val	Leu	Ile	Ala	Leu	Thr	Phe	Ile	Pro	
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gcg	ctg	ttg	ggt	gtg	ttt	ggt	ggt	cat	gcg	ttc	aag	ggc	aag	atc	cct	1171
Ala	Leu	Leu	Gly	Val	Phe	Gly	Gly	His	Ala	Phe	Lys	Gly	Lys	Ile	Pro	
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gga	att	ggt	gga	aac	cca	acg	cca	aag	cag	acg	tgg	gag	caa	gcg	ctt	1219
Gly	Ile	Gly	Gly	Asn	Pro	Thr	Pro	Lys	Gln	Thr	Trp	Glu	Gln	Ala	Leu	
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Asn	Arg	Arg	Ser	Lys	Gly	Arg	Ser	Trp	Val	Lys	Leu	Val	Gln	Lys	Ala	
	375					380					385					
ccg	ggt	ctt	gtg	gtg	gca	gtg	gtg	gtc	ttg	ggt	ctt	ggt	gcc	ttg	acc	1315
Pro	Gly	Leu	Val	Val	Ala	Val	Val	Val	Leu	Gly	Leu	Gly	Ala	Leu	Thr	
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Ile	Pro	Ala	Met	Asn	Leu	Gln	Leu	Ser	Leu	Pro	Ser	Asp	Ser	Thr	Ser	
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Asn	Ile	Asp	Thr													

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His Arg Asp Val Ile Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly

Item	Unit	Value
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95. Private		90.00
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98. Public		10.00
99. Private		90.00
100. Foreign		10.00

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Ile	Phe 210	Thr	Phe	Gly	Ser	Leu 215	Ile	Ala	Ala	Gly	Leu 220	Pro	Leu	Ile	Thr	
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Ala	Phe	Thr	Asp	Leu 245	Asn	Asn	Val	Thr	Pro 250	Val	Leu	Ala	Val	Met 255	Ile	
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Lys	Gly 355	Lys	Ile	Pro	Gly	Ile	Gly 360	Gly	Asn	Pro	Thr	Pro 365	Lys	Gln	Thr	
Trp	Glu 370	Gln	Ala	Leu	Asn	Arg 375	Arg	Ser	Lys	Gly	Arg 380	Ser	Trp	Val	Lys	
Leu 385	Val	Gln	Lys	Ala	Pro 390	Gly	Leu	Val	Val	Ala 395	Val	Val	Val	Leu	Gly 400	
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Ile 450	Val	Asp	Thr	His	Glu	Val 455	Asn	Ala	Asp	Ser	Thr 460	Ala	Leu	Gln	Pro	
Leu 465	Ile	Glu	Ala	Gln	Glu 470	Pro	Glu	Glu	Gly	Glu 475	Phe	Asp	Arg	Glu	Gln 480	
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 Thr Ala Ala Gln Ile Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys
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 Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val
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 Gly Ala Ala Phe Gly Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly
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 Gly Phe Val Asn Thr Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe
 625 630 635 640
 Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu
 645 650 655
 Val Thr Arg Met Arg Glu His Tyr Thr His His Asn Gly Lys Gly Gln
 660 665 670
 Pro Gly Ser Lys Tyr Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe
 675 680 685
 Thr Gln Gly Ser Arg Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala
 690 695 700
 Val Phe Val Ala Phe Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe
 705 710 715 720
 Gly Phe Ala Leu Gly Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg
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 Met Gly Leu Val Pro Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp
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 35 40 45
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 Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
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 Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
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 Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
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 Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
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 Met Ser Thr Ser Ile
 1 5
 aca aca gag aac aag aag aaa tct ggt cct cct cgc ttg atg aga atc 163
 Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro Arg Leu Met Arg Ile
 10 15 20
 ttt ctg ccc gcc ttg cta att tta gtt tgg ctt gta gga gct gga gtc 211
 Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu Val Gly Ala Gly Val
 25 30 35
 ggc ggt cct tat ttt ggc aag gtt agt gag gtc tcc tcc aac agc cag 259
 Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val Ser Ser Asn Ser Gln
 40 45 50
 acc aca tat ctg cca gaa tct gcc gat gcc act caa gta cag gaa cag 307

Thr	Thr	Tyr	Leu	Pro	Glu	Ser	Ala	Asp	Ala	Thr	Gln	Val	Gln	Glu	Gln		
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Leu	Gly	Asp	Phe	Thr	Asp	Ser	Glu	Ser	Ile	Pro	Ala	Ile	Val	Val	Met	85	
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gtc	agc	gat	gaa	ccc	tta	aca	cag	caa	gac	atc	aca	caa	ctc	aat	gaa	403	
Val	Ser	Asp	Glu	Pro	Leu	Thr	Gln	Gln	Asp	Ile	Thr	Gln	Leu	Asn	Glu	100	
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Leu	Phe	Ala	Leu	Thr	Val	Ala	Leu	Leu	Val	Val	Trp	Trp	Leu	Ala	Lys	225	
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Leu	Val	Ile	Gly	Ala	Ala	Thr	Asp	Tyr	Ser	Leu	Leu	Tyr	Val	Ala	Arg	260	
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Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile Ile Phe Ala Met Leu			
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Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe Val Phe Gly Arg Val			
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gcc ttt tgg ccc aag cga cca aaa tac gaa cct gaa aaa gcc cgt gcg			1171
Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro Glu Lys Ala Arg Ala			
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aaa aac gac atc ccc gcc agc ggg atc tgg tca aaa gtg gct gat tta			1219
Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser Lys Val Ala Asp Leu			
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gtg gag cag cat cct cgt gca atc tgg gta tct aca ctt att gtg ctt			1267
Val Glu Gln His Pro Arg Ala Ile Trp Val Ser Thr Leu Ile Val Leu			
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ctc ttg ggt gcg gct ttc gtt ccc aca cta aaa gcg gac ggt gtg tcc			1315
Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys Ala Asp Gly Val Ser			
	390	395	400
caa tcc gac cta gtt ctg ggt tcc tct gaa gca cgt gat ggc cag cag			1363
Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala Arg Asp Gly Gln Gln			
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gct tta ggc gaa cac ttc ccc ggt gga tcc ggc agt cct gct tat att			1411
Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly Ser Pro Ala Tyr Ile			
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atc gtt gat gaa aca cag gca gca cag gct gct gac gta gtc ctt aac			1459
Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala Asp Val Val Leu Asn			
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aac gac aat ttc gag act gta act gta act agt gct gac tcc ccc tct			1507
Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser Ala Asp Ser Pro Ser			
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Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val Pro Leu Gly Ser Gly			
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Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile Ser Ala Val Val Gly			
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Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp Ala Ser Ile His Asp			
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 Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val Ile Leu Val Ile Leu
 550 555 560 565

 atg ctg ttg ctg cgg tct att gtc gca cca ctc ctg cta gta gtc acc 1843
 Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu Leu Leu Val Val Thr
 570 575 580

 acc gtg gtg tct ttt gct act gct tta ggc gtg gct gct tta ctt ttc 1891
 Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val Ala Ala Leu Leu Phe
 585 590 595

 aat cac gtt ttc agt ttc cca gga gca gac ccc gca gta cct ctc tac 1939
 Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro Ala Val Pro Leu Tyr
 600 605 610

 gga ttt gta ttt tta gta gcc ttg ggc atc gac tac aac att ttc tta 1987
 Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp Tyr Asn Ile Phe Leu
 615 620 625

 gtc acc cga atc cgt gaa gaa acc aaa acc cac ggc aca aga ctt gga 2035
 Val Thr Arg Ile Arg Glu Thr Lys Thr His Gly Thr Arg Leu Gly
 630 635 640 645

 att ctt cga ggc ctg aca gta acc ggc gga gta att acc tca gct gga 2083
 Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val Ile Thr Ser Ala Gly
 650 655 660

 gta gtt ctc gcc gca acg ttc gca gca ctc tat gtc atc cca att cta 2131
 Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr Val Ile Pro Ile Leu
 665 670 675

 ttc ctg gca caa att gcc ttc att gtc gct ttt gga gtt ctt att gat 2179
 Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe Gly Val Leu Ile Asp
 680 685 690

 acc ctg ctc gtt cgc gcc ttc ttg gtg cct gct ttg ttc tac gac atc 2227
 Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala Leu Phe Tyr Asp Ile
 695 700 705

 gga ccg aaa atc tgg tgg ccg tca aaa ttg tcc aat cag aaa tac cag 2275
 Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser Asn Gln Lys Tyr Gln
 710 715 720 725

 aag cag cct cag cta tgacacacca aaattcgccct ctc 2313
 Lys Gln Pro Gln Leu
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<210> 358

<211> 730

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

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 20 25 30

Val Gly Ala Gly Val Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val
 35 40 45
 Ser Ser Asn Ser Gln Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr
 50 55 60
 Gln Val Gln Glu Gln Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro
 65 70 75 80
 Ala Ile Val Val Met Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile
 85 90 95
 Thr Gln Leu Asn Glu Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val
 100 105 110
 Ser Asp Glu Val Ser Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val
 115 120 125
 Gln Val Phe Val Pro Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val
 130 135 140
 Glu Lys Leu Ser Glu Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser
 145 150 155 160
 Thr Tyr Val Thr Gly Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala
 165 170 175
 Phe Ala Gly Ile Asp Gly Leu Leu Leu Ala Val Ala Leu Ala Val
 180 185 190
 Leu Val Ile Leu Val Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala
 195 200 205
 Val Leu Ala Thr Ser Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val
 210 215 220
 Trp Trp Leu Ala Lys Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln
 225 230 235 240
 Gly Ile Leu Phe Ile Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu
 245 250 255
 Leu Tyr Val Ala Arg Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys
 260 265 270
 Gly Ile Ala Thr Gly Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu
 275 280 285
 Ala Ser Gly Ser Thr Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser
 290 295 300
 Asp Leu Lys Ser Asn Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile
 305 310 315 320
 Ile Phe Ala Met Leu Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe
 325 330 335
 Val Phe Gly Arg Val Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro
 340 345 350

Glu Lys Ala Arg Ala Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser
 355 360 365
 Lys Val Ala Asp Leu Val Glu Gln His Pro Arg Ala Ile Trp Val Ser
 370 375 380
 Thr Leu Ile Val Leu Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys
 385 390 395 400
 Ala Asp Gly Val Ser Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala
 405 410 415
 Arg Asp Gly Gln Gln Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly
 420 425 430
 Ser Pro Ala Tyr Ile Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala
 435 440 445
 Asp Val Val Leu Asn Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser
 450 455 460
 Ala Asp Ser Pro Ser Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val
 465 470 475 480
 Pro Leu Gly Ser Gly Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln
 485 490 495
 Val Leu Leu Gln Ala Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala
 500 505 510
 Gln Lys Ala Ile Arg Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile
 515 520 525
 Ser Ala Val Val Gly Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp
 530 535 540
 Ala Ser Ile His Asp Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val
 545 550 555 560
 Ile Leu Val Ile Leu Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu
 565 570 575
 Leu Leu Val Val Thr Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val
 580 585 590
 Ala Ala Leu Leu Phe Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro
 595 600 605
 Ala Val Pro Leu Tyr Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp
 610 615 620
 Tyr Asn Ile Phe Leu Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His
 625 630 635 640
 Gly Thr Arg Leu Gly Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val
 645 650 655
 Ile Thr Ser Ala Gly Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr
 660 665 670
 Val Ile Pro Ile Leu Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe

675 680 685

Gly Val Leu Ile Asp Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala
690 695 700

Leu Phe Tyr Asp Ile Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser
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Asn Gln Lys Tyr Gln Lys Gln Pro Gln Leu
725 730

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<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXS02586

<400> 359
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gatgccacca tcatccgat gctgcttgtc ccccgccgtg atg cac ctg ctt cgc 115
Met His Leu Leu Arg
1 5

gac gac aac tgg tgg gca ccc ggc ttc gtt aaa aag gcc tac acc gtc 163
Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys Lys Ala Tyr Thr Val
10 15 20

atg ggt cac ggc tct gag gtg gag gaa gca cct cgc cca acc acc cgt 211
Met Gly His Gly Ser Glu Val Glu Glu Ala Pro Arg Pro Thr Thr Arg
25 30 35

cgc ctc aac gac gat gag gaa gtc acc gtg cat gaa gca gtt gtc gct 259
Arg Leu Asn Asp Asp Glu Glu Val Thr Val His Glu Ala Val Val Ala
40 45 50

ggc gat acc gtg gca tct cgc ggt ggt ttg agc acg cag gaa aac cgt 307
Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser Thr Gln Glu Asn Arg
55 60 65

gat ctg gtg tcc ttc gtg gaa ctt aag gct cgt ttg gaa aag cgc agg 355
Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg Leu Glu Lys Arg Arg
70 75 80 85

ctt gag gat cta gat taaatctatg cgaggatttt tca 393
Leu Glu Asp Leu Asp
90

<210> 360
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 360
Met His Leu Leu Arg Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys

<400> 361																
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ttgttatcca accgccacaa ttcccaggag taatccaccc																115
											gtg	ttt	tct	aaa	tgg	
											Val	Phe	Ser	Lys	Trp	
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ggc cac ttt gct tac aga ttt agg cgc att gtt ccg tta gtc gtc atc																163
Gly	His	Phe	Ala	Tyr	Arg	Phe	Arg	Arg	Ile	Val	Pro	Leu	Val	Val	Ile	
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gcc gcg att ttg gct ttg ttt gtc att ttc gcc acc aag ctg gcc gac																211
Ala	Ala	Ile	Leu	Ala	Leu	Phe	Val	Ile	Phe	Gly	Thr	Lys	Leu	Gly	Asp	
			25					30					35			
cgc atg agc cag gaa gga tgg gat gat cct ggt tct tcc tcg acc gct																259
Arg	Met	Ser	Gln	Glu	Gly	Trp	Asp	Asp	Pro	Gly	Ser	Ser	Ser	Thr	Ala	
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gcg gcg cgc atc gag ttg gag acc ttt ggg cgt gac aat gac gcc gat																307
Ala	Ala	Arg	Ile	Glu	Leu	Glu	Thr	Phe	Gly	Arg	Asp	Asn	Asp	Gly	Asp	
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gtc gtg ttg ctg ttt act gcg cct gaa gcc act tct ttc gat gat gca																355
Val	Val	Leu	Leu	Phe	Thr	Ala	Pro	Glu	Gly	Thr	Ser	Phe	Asp	Asp	Ala	
		70			75					80					85	
gag gtg ttc tcc agc atc tct ggc tac tta gat ggg cta atc gag aac																403
Glu	Val	Phe	Ser	Ser	Ile	Ser	Gly	Tyr	Leu	Asp	Gly	Leu	Ile	Glu	Asn	
				90					95					100		
aac cct gat gaa gtc agc cac atc aac agc tac ttt gac act cgt aat																451
Asn	Pro	Asp	Glu	Val	Ser	His	Ile	Asn	Ser	Tyr	Phe	Asp	Thr	Arg	Asn	

105	110	115	
caa aat ctc ctc agc aaa gac ggc acc caa acc ttt gca gct ctc ggg Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr Phe Ala Ala Leu Gly 120 125 130			499
ctc aaa ggt gac ggc gag caa acg ctg aag gac ttc cgg gag att gaa Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp Phe Arg Glu Ile Glu 135 140 145			547
gat cag ctc cat ccg gac aac ctt gcc ggt ggc gtc acc act gag gtc Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly Val Thr Thr Glu Val 150 155 160 165			595
gcg ggt gcc acc gct gta gcc gac gca ctc gat gag ggc atg gct ggc Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp Glu Gly Met Ala Gly 170 175 180			643
gat att tca cgc gcc gaa gtt ttt gcg ctg cct ttc gtg gct atc ttg Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro Phe Val Ala Ile Leu 185 190 195			691
ctg ctc atc gtg ttt ggc tca gtt gtt gcc gcg gcg atg cca ttg atc Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala Ala Met Pro Leu Ile 200 205 210			739
gtg ggc att ttg tcc atc ttg ggt tcg ctg ggc atc ttg gca att ttg Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly Ile Leu Ala Ile Leu 215 220 225			787
gct gga ttc ttc cag gtc aac gta ttt gca caa tct gtt gtg acc ctt Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln Ser Val Val Thr Leu 230 235 240 245			835
ctg ggc ttg ggt ctt gcc att gac tat ggc tta ttc atg gtc tct cgt Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu Phe Met Val Ser Arg 250 255 260			883
ttc cgt gag gaa atg gat aag ggc acc ccg gtt gaa cag gct gtt gcc Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val Glu Gln Ala Val Ala 265 270 275			931
acc act acg gcg acc gcg ggt aag act gtg gtg ttc tct gca gcg atg Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val Phe Ser Ala Ala Met 280 285 290			979
gtg gct gtg gcg ctg tcc ggg ttg ttt gtt ttc cca cag gct ttc ttg Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe Pro Gln Ala Phe Leu 295 300 305			1027
aag tcg gtg gca ttc ggt gcg att tcc gcg gtt ggc ctt gct gct ttg Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val Gly Leu Ala Ala Leu 310 315 320 325			1075
atg tcg gtg acg gtg ttg ccg tcg ctg ttc agc atg ttg ggt aag aat Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser Met Leu Gly Lys Asn 330 335 340			1123
atc gat aag tgg agt ttg cgt cgc act gct cga aca gcg cgc cgt ttg Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg Thr Ala Arg Arg Leu 345 350 355			1171

gaa gac acc att tgg tac cgc gtg ccg gca tgg gca atg cgc cat gcc 1219
 Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp Ala Met Arg His Ala
 360 365 370

aag gca gtg acc gtg ggc gtc gta ttg ctc ttg ctt gct ctt aca gtg 1267
 Lys Ala Val Thr Val Gly Val Val Leu Leu Leu Leu Ala Leu Thr Val
 375 380 385

ccg ttg acg ggc gtg aaa ttc ggc ggc atc aat gaa acg tat ctg cca 1315
 Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn Glu Thr Tyr Leu Pro
 390 395 400 405

cca gct aac gac acc cgc gtc gcc caa gag cgt ttc gac gag gcg ttt 1363
 Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg Phe Asp Glu Ala Phe
 410 415 420

ccc gcc ttc cgc acc gag ccg gtc aag ctt gtg gtc acc ggg gcg gac 1411
 Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val Val Thr Gly Ala Asp
 425 430 435

aac aac cag ctg atc gat atc tat gtt cag gcc aac gaa gtt gag gga 1459
 Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala Asn Glu Val Glu Gly
 440 445 450

ctg aca gat cgt ttc acc gca ggt gcg act acc gat gat ggc acc acg 1507
 Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr Asp Asp Gly Thr Thr
 455 460 465

gtg ttg tct act ggt att cag gat cgt tcc ctc aat gag cag gta gtg 1555
 Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu Asn Glu Gln Val Val
 470 475 480 485

gag cag ctt cgc gct att tcc gtc cct gag ggc gtt gag gtg cag atc 1603
 Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly Val Glu Val Gln Ile
 490 495 500

ggt ggc act cca gcc atg gag atc gaa tcc att gag gcg ctc ttt gaa 1651
 Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile Glu Ala Leu Phe Glu
 505 510 515

aag ctc ctc tgg atg gct ctc tac att gtg ctg gcc act ttc atc ctc 1699
 Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu Ala Thr Phe Ile Leu
 520 525 530

atg gca ttg gta ttt ggt tcc gtg att ttg ccg gcg aag gcc atc atc 1747
 Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro Ala Lys Ala Ile Ile
 535 540 545

atg acc att ctg ggt atg ggt gcc acc ttg ggt att ctc acc ttg atg 1795
 Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly Ile Leu Thr Leu Met
 550 555 560 565

ttc gtc gat ggc gtg ggt gcc agc gca ttg aac ttc tcc cct ggc cca 1843
 Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn Phe Ser Pro Gly Pro
 570 575 580

ctg atg agt cca gtg ctg gtg ctg atc atg gct att att tac gga ctt 1891
 Leu Met Ser Pro Val Leu Val Leu Ile Met Ala Ile Ile Tyr Gly Leu
 585 590 595

tcc acc gac tat gag gtg ttc ctg gta tct cgc atg gtg gag gcc cgc 1939
 Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg Met Val Glu Ala Arg
 600 605 610

gat aaa ggc gaa tcc acc gac gac gcc atc aga tac ggc act gca cac 1987
 Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg Tyr Gly Thr Ala His
 615 620 625

acc gga tct atc atc acc gcg gcc gca ctg atc atg att gtg gtc tgt 2035
 Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile Met Ile Val Val Cys
 630 635 640 645

gga gcg ttt ggt ttc tct gag atc gtc atg atg aag tac atc gcg ttc 2083
 Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met Lys Tyr Ile Ala Phe
 650 655 660

ggc atg atc gca gcg ctg att ctg gat gcc acc atc atc cgc atg ctg 2131
 Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr Ile Ile Arg Met Leu
 665 670 675

ctt gtc ccc cgc cgt gat gca cct gct tcg cga cga caa ctg gtg ggc 2179
 Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg Arg Gln Leu Val Gly
 680 685 690

acc cgg ctt cgt taaaaaggcc tacaccgtca tgg 2214
 Thr Arg Leu Arg
 695

<210> 362

<211> 697

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

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Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly
 35 40 45

Ser Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg
 50 55 60

Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr
 65 70 75 80

Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp
 85 90 95

Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr
 100 105 110

Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr
 115 120 125

Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp
 130 135 140

Phe 145	Arg	Glu	Ile	Glu	Asp 150	Gln	Leu	His	Pro	Asp 155	Asn	Leu	Ala	Gly	Gly 160
Val	Thr	Thr	Glu	Val 165	Ala	Gly	Ala	Thr	Ala 170	Val	Ala	Asp	Ala	Leu 175	Asp
Glu	Gly	Met	Ala 180	Gly	Asp	Ile	Ser	Arg 185	Ala	Glu	Val	Phe	Ala 190	Leu	Pro
Phe	Val	Ala 195	Ile	Leu	Leu	Leu	Ile 200	Val	Phe	Gly	Ser	Val 205	Val	Ala	Ala
Ala	Met 210	Pro	Leu	Ile	Val	Gly 215	Ile	Leu	Ser	Ile	Leu 220	Gly	Ser	Leu	Gly
Ile 225	Leu	Ala	Ile	Leu	Ala 230	Gly	Phe	Phe	Gln	Val 235	Asn	Val	Phe	Ala	Gln 240
Ser	Val	Val	Thr	Leu 245	Leu	Gly	Leu	Gly	Leu 250	Ala	Ile	Asp	Tyr	Gly 255	Leu
Phe	Met	Val	Ser 260	Arg	Phe	Arg	Glu	Glu 265	Met	Asp	Lys	Gly	Thr 270	Pro	Val
Glu	Gln	Ala 275	Val	Ala	Thr	Thr	Thr 280	Ala	Thr	Ala	Gly	Lys 285	Thr	Val	Val
Phe	Ser 290	Ala	Ala	Met	Val	Ala 295	Val	Ala	Leu	Ser	Gly 300	Leu	Phe	Val	Phe
Pro 305	Gln	Ala	Phe	Leu	Lys 310	Ser	Val	Ala	Phe	Gly 315	Ala	Ile	Ser	Ala	Val 320
Gly	Leu	Ala	Ala	Leu 325	Met	Ser	Val	Thr	Val 330	Leu	Pro	Ser	Leu	Phe 335	Ser
Met	Leu	Gly	Lys 340	Asn	Ile	Asp	Lys	Trp 345	Ser	Leu	Arg	Arg	Thr 350	Ala	Arg
Thr	Ala	Arg 355	Arg	Leu	Glu	Asp	Thr 360	Ile	Trp	Tyr	Arg	Val 365	Pro	Ala	Trp
Ala	Met 370	Arg	His	Ala	Lys	Ala 375	Val	Thr	Val	Gly	Val 380	Val	Leu	Leu	Leu
Leu 385	Ala	Leu	Thr	Val	Pro 390	Leu	Thr	Gly	Val	Lys 395	Phe	Gly	Gly	Ile	Asn 400
Glu	Thr	Tyr	Leu	Pro 405	Pro	Ala	Asn	Asp	Thr 410	Arg	Val	Ala	Gln	Glu 415	Arg
Phe	Asp	Glu	Ala 420	Phe	Pro	Ala	Phe	Arg 425	Thr	Glu	Pro	Val	Lys 430	Leu	Val
Val	Thr	Gly 435	Ala	Asp	Asn	Asn	Gln 440	Leu	Ile	Asp	Ile	Tyr 445	Val	Gln	Ala
Asn	Glu 450	Val	Glu	Gly	Leu	Thr 455	Asp	Arg	Phe	Thr	Ala 460	Gly	Ala	Thr	Thr

Asp Asp Gly Thr Thr Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu
 465 470 475 480
 Asn Glu Gln Val Val Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly
 485 490 495
 Val Glu Val Gln Ile Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile
 500 505 510
 Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu
 515 520 525
 Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro
 530 535 540
 Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly
 545 550 555 560
 Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn
 565 570 575
 Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala
 580 585 590
 Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg
 595 600 605
 Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg
 610 615 620
 Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile
 625 630 635 640
 Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met
 645 650 655
 Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr
 660 665 670
 Ile Ile Arg Met Leu Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg
 675 680 685
 Arg Gln Leu Val Gly Thr Arg Leu Arg
 690 695

<210> 363

<211> 729

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(706)

<223> RXS03042

<400> 363

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 Leu Val Leu Ala Phe

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ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg			163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala			
	10	20	
gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg			211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val			
	25	35	
gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca			259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro			
	40	50	
ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg			307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu			
	55	65	
gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc			355
Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe			
	70	85	
acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac			403
Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His			
	90	100	
ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc			451
Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe			
	105	115	
gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt			499
Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe			
	120	130	
gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg			547
Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met			
	135	145	
att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta			595
Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu			
	150	165	
cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag			643
Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu			
	170	180	
ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat			691
Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn			
	185	195	
gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta			729
Val Gly Val Gly Ala			
	200		

<210> 364

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Leu Val Leu Ala Phe Leu Val Leu Leu Val Phe Arg Ser Ile Trp
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 Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
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 Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45
 Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
 50 55 60
 Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
 65 70 75 80
 Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
 85 90 95
 Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
 100 105 110
 Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
 115 120 125
 Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
 130 135 140
 Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
 145 150 155 160
 Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
 165 170 175
 Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
 180 185 190
 Glu Leu Lys Glu Asn Val Gly Val Gly Ala
 195 200

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 <223> RXS03075

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agcccagaag aacagtcaac tcctagatta aaggataatc gtg gcg aaa ttc ctg 115
 Val Ala Lys Phe Leu
 1 5

tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg 163
 Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala
 10 15 20

gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat	211
Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr	
25 30 35	
gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc	259
Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val	
40 45 50	
acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca	307
Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala	
55 60 65	
aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag	355
Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys	
70 75 80 85	
acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat	403
Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp	
90 95 100	
gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat	451
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp	
105 110 115	
cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg	499
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu	
120 125 130	
gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg	547
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser	
135 140 145	
att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act	595
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr	
150 155 160 165	
ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag	643
Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys	
170 175 180	
gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc	691
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val	
185 190 195	
tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc	739
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr	
200 205 210	
tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc	787
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr	
215 220 225	
ttc ggt tcg ttc atc gct gcc ggt atg ccg ctg atc tct	826
Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser	
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<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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 Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
 35 40 45
 Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
 50 55 60
 Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65 70 75 80
 Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
 85 90 95
 Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
 100 105 110
 Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
 115 120 125
 Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
 130 135 140
 Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
 145 150 155 160
 Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
 165 170 175
 Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
 180 185 190
 Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
 195 200 205
 Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
 210 215 220
 Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
 225 230 235 240
 Ile Ser

<210> 367

<211> 983

<212> DNA

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<223> RXS03124

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Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln	
20 25 30	
act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc	144
Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg	
35 40 45	
acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc	192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly	
50 55 60	
act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct	240
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala	
65 70 75 80	
ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc	288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala	
85 90 95	
att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc	336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser	
100 105 110	
ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca	384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala	
115 120 125	
cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg	432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr	
130 135 140	
atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac	480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr	
145 150 155 160	
ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc	528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr	
165 170 175	
aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc	576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr	
180 185 190	
gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc	624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly	
195 200 205	
cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag	672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu	
210 215 220	
gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac	720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn	
225 230 235 240	

GENE TEST

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			20					25					30			
Thr	Gly	Ala	Asn	Asp	Leu	Glu	Pro	Lys	Glu	Leu	Ala	Glu	Arg	Leu	Arg	
		35					40					45				
Thr	Met	Pro	Leu	Ala	Ala	Arg	Ala	His	Ala	Met	Gly	Met	Ala	Val	Gly	
	50					55					60					
Thr	Ala	Gly	Ser	Ala	Val	Val	Phe	Ala	Gly	Thr	Thr	Val	Leu	Ile	Ala	
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Leu	Val	Ala	Leu	Ser	Ile	Ile	Asn	Ile	Pro	Phe	Leu	Thr	Val	Met	Ala	
				85					90					95		
Ile	Ala	Ala	Ala	Ile	Thr	Val	Ala	Ile	Ala	Val	Leu	Val	Ala	Leu	Ser	
			100					105					110			
Phe	Leu	Pro	Ala	Leu	Leu	Gly	Leu	Leu	Gly	Thr	Arg	Ile	Phe	Ala	Ala	
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Arg	Val	Pro	Gly	Pro	Lys	Val	Pro	Asp	Pro	Glu	Asp	Glu	Lys	Pro	Thr	
	130					135					140					
Met	Gly	Leu	Lys	Trp	Val	Arg	Leu	Val	Arg	Lys	Met	Pro	Val	Ala	Tyr	
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				165					170					175		

Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
305 310 315 320

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
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271

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Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
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Asp Asp Pro Gln Pro Leu Leu Cys Phe
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<223> RXA00596

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Met Leu Asn Ala Leu
1 5
aaa ttc atc cca tgg ctg atc ggc cag att ttc ctc tct ggc ttc agc 163
Lys Phe Ile Pro Trp Leu Ile Gly Gln Ile Phe Leu Ser Gly Phe Ser
10 15 20
gtg atc acc gct gcg gta aaa aag gac acc ggc ttc aac ccc gtt gtt 211
Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly Phe Asn Pro Val Val
25 30 35
atc cgc tac cca ctt cga gtg acc acg gac ttc cag atc gca gcc ctg 259
Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe Gln Ile Ala Ala Leu
40 45 50
tca acg tgc atc acc gcg act cct tcc acc ctg tcc ctt ggc cta cgc 307
Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu Ser Leu Gly Leu Arg
55 60 65
gaa ccc cgc aag ccc ggc gac ccc acc att ttg ctg atc caa gca gtg 355
Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu Leu Ile Gln Ala Val
70 75 80 85

ttt ggt tcc gat cca gta gaa gtt ttt gaa tcc atc gcc gat atg gaa 403
 Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser Ile Ala Asp Met Glu
 90 95 100

caa cgc ctc gtc cct tcg gtc gct tca att gac cac ggc gtc cca ggc 451
 Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp His Gly Val Pro Gly
 105 110 115

caa ggc cct tac aag gag atc cgc ccc agc gat gct gag tgg cca agt 499
 Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp Ala Glu Trp Pro Ser
 120 125 130

cgc gag atc gct gac acc gcc caa aac acc gtc agc caa gac aag agg 547
 Arg Glu Ile Ala Asp Thr Ala Gln Asn Thr Val Ser Gln Asp Lys Arg
 135 140 145

gag ttt taaaacaaca tgactgcttt tgg 576
 Glu Phe
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 <213> Corynebacterium glutamicum

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Phe Asn Pro Val Val Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe
 35 40 45

Gln Ile Ala Ala Leu Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu
 50 55 60

Ser Leu Gly Leu Arg Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu
 65 70 75 80

Leu Ile Gln Ala Val Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser
 85 90 95

Ile Ala Asp Met Glu Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp
 100 105 110

His Gly Val Pro Gly Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp
 115 120 125

Ala Glu Trp Pro Ser Arg Glu Ile Ala Asp Thr Ala Gln Asn Thr Val
 130 135 140

Ser Gln Asp Lys Arg Glu Phe
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 <212> DNA

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<223> RXA02079

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 Met Ser Glu Ala Phe
 1 5

gat gca acc aaa gtg cgc aaa gct gtg ctg acc gtc gcg ctg ctt aac 163
 Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr Val Ala Leu Leu Asn
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ttc gct tat ttc ttt gta gaa ttc ttt att gca tta agc gca ggc tcc 211
 Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala Leu Ser Ala Gly Ser
 25 30 35

gtt tct cta ctg gct gac agt gtc gat ttt ctt gaa gac acc tcc atc 259
 Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu Glu Asp Thr Ser Ile
 40 45 50

aac ctg ctg att ttc att gcc cta gga tgg ccg ttg gcg agg cgc gca 307
 Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro Leu Ala Arg Arg Ala
 55 60 65

gtg atg ggc aaa ctt atg gcg att gtg att ctt gca cct gct gct ttt 355
 Val Met Gly Lys Leu Met Ala Ile Val Ile Leu Ala Pro Ala Ala Phe
 70 75 80 85

gct gcg tgg gca gcg att caa cgg ttt tcc gca ccg caa gcg ccc gaa 403
 Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala Pro Gln Ala Pro Glu
 90 95 100

gtg ttt ccg atc atc gtc gct tct ctg ggc gcc gtc gtg atc aac ggc 451
 Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala Val Val Ile Asn Gly
 105 110 115

gcg agt gcc atc att att tct cga gtg cga caa cat ggt ggc tgc ctt 499
 Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln His Gly Gly Ser Leu
 120 125 130

ggc caa gct gcc ttc cta tcc gcc cga aat gac gtc ctg atc aac att 547
 Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp Val Leu Ile Asn Ile
 135 140 145

gcc atc atc atg atg gcc tta att acc gca tgg acg acg tct gga tgg 595
 Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp Thr Thr Ser Gly Trp
 150 155 160 165

cca gat ttg atc cta ggt tgt ttc atc att ctg ctg gca ctg cac gcc 643
 Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu Leu Ala Leu His Ala
 170 175 180

gct cac gag gtg tgg gaa gtc agt gag gaa gaa cgc ctg gcc tcc aaa 691
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738

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Leu	Ser	Ala	Gly	Ser	Val	Ser	Leu	Leu	Ala	Asp	Ser	Val	Asp	Phe	Leu	
		35					40					45				
Glu	Asp	Thr	Ser	Ile	Asn	Leu	Leu	Ile	Phe	Ile	Ala	Leu	Gly	Trp	Pro	
	50					55					60					
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65					70					75					80	
Ala	Pro	Ala	Ala	Phe	Ala	Ala	Trp	Ala	Ala	Ile	Gln	Arg	Phe	Ser	Ala	
				85					90					95		
Pro	Gln	Ala	Pro	Glu	Val	Phe	Pro	Ile	Ile	Val	Ala	Ser	Leu	Gly	Ala	
			100					105					110			
Val	Val	Ile	Asn	Gly	Ala	Ser	Ala	Ile	Ile	Ile	Ser	Arg	Val	Arg	Gln	
		115					120					125				
His	Gly	Gly	Ser	Leu	Gly	Gln	Ala	Ala	Phe	Leu	Ser	Ala	Arg	Asn	Asp	
	130					135					140					
Val	Leu	Ile	Asn	Ile	Ala	Ile	Ile	Met	Met	Ala	Leu	Ile	Thr	Ala	Trp	
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				165					170					175		
Leu	Ala	Leu	His	Ala	Ala	His	Glu	Val	Trp	Glu	Val	Ser	Glu	Glu	Glu	
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                               Val Thr Gln Leu Asn
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acc aaa ggc gtt gtt ctg caa ggg tgg gat cca gaa gat cct gaa cat 163
Thr Lys Gly Val Val Leu Gln Gly Trp Asp Pro Glu Asp Pro Glu His
                               10                               15                               20

tgg gac tcg aaa att gca tgg cga acc ctg tgg att acc acc ttc tcc 211
Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp Ile Thr Thr Phe Ser
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atg att att ggg ttc tgc gtg tgg tat ttg gtt tct gcc atc gct ccc 259
Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val Ser Ala Ile Ala Pro
                               40                               45                               50

cta ctc aat cga att gga ttt gat ctc tca gca ggt cag ctt tat tgg 307
Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala Gly Gln Leu Tyr Trp
                               55                               60                               65

ctc gca tct atc ccc ggt ttg gcc ggc gga tta atc cga ttg att tac 355
Leu Ala Ser Ile Pro Gly Leu Ala Gly Gly Leu Ile Arg Leu Ile Tyr
                               70                               75                               80                               85

atg ttc ctt cca ccg att ctt gga acc cgc aaa ttg gtc gga att tcc 403
Met Phe Leu Pro Pro Ile Leu Gly Thr Arg Lys Leu Val Gly Ile Ser
                               90                               95                               100

tcc ggt cta ttt ttg atc ccc atg ttt ggg tgg ttc ctg gct gtc caa 451
Ser Gly Leu Phe Leu Ile Pro Met Phe Gly Trp Phe Leu Ala Val Gln
                               105                               110                               115

gat tca agc act ccc tac tgg tgg ctt ctc aca ctc gct gca ctc act 499
Asp Ser Ser Thr Pro Tyr Trp Trp Leu Leu Thr Leu Ala Ala Leu Thr
                               120                               125                               130

ggc att ggt ggt ggc gtg ttc tct gga tat atg ccg tcc acg gga tac 547
Gly Ile Gly Gly Gly Val Phe Ser Gly Tyr Met Pro Ser Thr Gly Tyr
                               135                               140                               145

ttc ttc ccc aag gca aaa tcg ggc act gcg ctg ggc att cag gca ggt 595
Phe Phe Pro Lys Ala Lys Ser Gly Thr Ala Leu Gly Ile Gln Ala Gly
                               150                               155                               160                               165

atc ggc aac ctc ggc gtc tcg ata att cag ttc atg ggc cca tgg gtc 643
Ile Gly Asn Leu Gly Val Ser Ile Ile Gln Phe Met Gly Pro Trp Val
                               170                               175                               180

atg ggt ttc ggt ctg ctg ggc att ggt ttc ctc acc ccg cag cgc acc 691
Met Gly Phe Gly Leu Leu Gly Ile Gly Phe Leu Thr Pro Gln Arg Thr
                               185                               190                               195

att gaa ggc acc acg gtg ttt gtg cac aat gct gcg att gtg ttg gtc 739
Ile Glu Gly Thr Thr Val Phe Val His Asn Ala Ala Ile Val Leu Val
                               200                               205                               210

ccg tgg act att ctc gcg gcc gtt tta tcc ttc ctg ttt ctt aaa gat 787

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Pro	Trp	Thr	Ile	Leu	Ala	Ala	Val	Leu	Ser	Phe	Leu	Phe	Leu	Lys	Asp		
215						220					225						
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Val	Pro	Val	Thr	Ala	Asn	Phe	Arg	Gln	Gln	Ile	Asp	Ile	Phe	Gly	Asn		
230					235					240					245		
aag	aac	aca	tgg	att	ttg	tcc	att	atc	tac	ttg	atg	aca	ttc	ggg	gcc	883	
Lys	Asn	Thr	Trp	Ile	Leu	Ser	Ile	Ile	Tyr	Leu	Met	Thr	Phe	Gly	Ala		
				250					255						260		
ttc	gcc	ggg	ttc	gcc	gcg	cag	ttc	ggg	ctg	atc	atc	aac	aac	aac	ttc	931	
Phe	Ala	Gly	Phe	Ala	Ala	Gln	Phe	Gly	Leu	Ile	Ile	Asn	Asn	Asn	Phe		
			265					270						275			
ggc	atc	gct	tcc	ccg	atg	gca	gag	act	tat	cca	gct	gag	atg	ctt	cac	979	
Gly	Ile	Ala	Ser	Pro	Met	Ala	Glu	Thr	Tyr	Pro	Ala	Glu	Met	Leu	His		
		280					285					290					
gcc	ggg	gct	acg	ttc	gcg	ttt	ctt	gga	cct	ttg	att	ggg	gct	ttg	gtg	1027	
Ala	Gly	Ala	Thr	Phe	Ala	Phe	Leu	Gly	Pro	Leu	Ile	Gly	Ala	Leu	Val		
		295					300					305					
cgt	gct	gca	tgg	ggg	cca	ctg	tgt	gac	aga	ttc	ggg	gga	gct	atc	tgg	1075	
Arg	Ala	Ala	Trp	Gly	Pro	Leu	Cys	Asp	Arg	Phe	Gly	Gly	Ala	Ile	Trp		
310					315					320					325		
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Thr	Phe	Val	Gly	Gly	Ile	Gly	Met	Thr	Ile	Ala	Thr	Ala	Ala	Ala	Ala		
				330					335						340		
atc	ttc	cta	agc	aga	gcg	gag	aca	cct	gat	gat	ttc	tgg	cca	ttc	ctg	1171	
Ile	Phe	Leu	Ser	Arg	Ala	Glu	Thr	Pro	Asp	Asp	Phe	Trp	Pro	Phe	Leu		
			345					350						355			
tgg	tcc	atg	ctt	gcc	ctg	ttc	ttc	ttc	acc	ggg	ctg	ggc	aat	gct	ggc	1219	
Trp	Ser	Met	Leu	Ala	Leu	Phe	Phe	Phe	Thr	Gly	Leu	Gly	Asn	Ala	Gly		
			360				365					370					
acc	ttc	aaa	caa	atg	ccc	atg	att	ttg	cct	aaa	cgc	caa	gca	ggg	ggc	1267	
Thr	Phe	Lys	Gln	Met	Pro	Met	Ile	Leu	Pro	Lys	Arg	Gln	Ala	Gly	Gly		
		375				380					385						
gtg	atc	ggc	tgg	acc	ggg	gcc	att	ggg	gcc	ttc	ggc	ccc	ttc	att	gtc	1315	
Val	Ile	Gly	Trp	Thr	Gly	Ala	Ile	Gly	Ala	Phe	Gly	Pro	Phe	Ile	Val		
390						395				400					405		
ggg	gtc	ttg	ctc	tcc	ttc	act	cca	act	gtc	gcg	ttc	ttc	tgg	ggc	tgc	1363	
Gly	Val	Leu	Leu	Ser	Phe	Thr	Pro	Thr	Val	Ala	Phe	Phe	Trp	Gly	Cys		
				410					415					420			
gtg	gtg	ttc	ttc	atc	atc	gcc	acc	gct	ttg	acc	tgg	atc	tac	tac	gcc	1411	
Val	Val	Phe	Phe	Ile	Ile	Ala	Thr	Ala	Leu	Thr	Trp	Ile	Tyr	Tyr	Ala		
			425					430					435				
cgc	ccg	aac	gct	cca	ttc	ccg	gga	taa	acc	gaaa	ggcca	atcca	tga			1458	
Arg	Pro	Asn	Ala	Pro	Phe	Pro	Gly										
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<213> Corynebacterium glutamicum

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Ile Gly Ala Leu Val Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe
305 310 315 320

Gly Gly Ala Ile Trp Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala
325 330 335

Thr Ala Ala Ala Ala Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp
340 345 350

Phe Trp Pro Phe Leu Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly
355 360 365

Leu Gly Asn Ala Gly Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys
370 375 380

Arg Gln Ala Gly Gly Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe
385 390 395 400

Gly Pro Phe Ile Val Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala
405 410 415

Phe Phe Trp Gly Cys Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr
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Trp Ile Tyr Tyr Ala Arg Pro Asn Ala Pro Phe Pro Gly
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<210> 377

<211> 738

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(715)

<223> RXA02079

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Met Ser Glu Ala Phe
1 5

gat gca acc aaa gtg cgc aaa gct gtg ctc acc gtc gcg ctg ctt aac 163
Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr Val Ala Leu Leu Asn
10 15 20

ttc gct tat ttc ttt gta gaa ttc ttt att gca tta agc gca ggc tcc 211
Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala Leu Ser Ala Gly Ser
25 30 35

gtt tct cta ctg gct gac agt gtc gat ttt ctt gaa gac acc tcc atc 259
Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu Glu Asp Thr Ser Ile
40 45 50

aac ctg ctc att ttc att gcc cta gga tgg ccg ttg gcg agg cgc gca 307
Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro Leu Ala Arg Arg Ala
55 60 65

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gtg atg ggc aaa ctt atg gcg att gtg att ctt gca cct gct gct ttt 355
Val Met Gly Lys Leu Met Ala Ile Val Ile Leu Ala Pro Ala Ala Phe
  70                75                80                85

gct gcg tgg gca gcg att caa cgg ttt tcc gca ccg caa gcg ccc gaa 403
Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala Pro Gln Ala Pro Glu
                90                95                100

gtg ttt ccg atc atc gtc gct tct ctg ggc gcc gtc gtg atc aac ggc 451
Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala Val Val Ile Asn Gly
                105                110                115

gcg agt gcc atc att att tct cga gtg cga caa cat ggt gcc tcg ctt 499
Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln His Gly Gly Ser Leu
                120                125                130

ggc caa gct gcc ttc cta tcc gcc cga aat gac gtc ctg atc aac att 547
Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp Val Leu Ile Asn Ile
                135                140                145

gcc atc atc atg atg gcc tta att acc gca tgg acg acg tct gga tgg 595
Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp Thr Thr Ser Gly Trp
                150                155                160                165

cca gat ttg atc cta ggt tgt ttc atc att ctg ctc gca ctg cac gcc 643
Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu Leu Ala Leu His Ala
                170                175                180

gct cac gag gtg tgg gaa gtc agt gag gaa gaa cgc ctc gcc tcc aaa 691
Ala His Glu Val Trp Glu Val Ser Glu Glu Glu Arg Leu Ala Ser Lys
                185                190                195

gcc ctt gct ggg gaa gcc atc gat taggggagca gtatgagctt ttc 738
Ala Leu Ala Gly Glu Ala Ile Asp
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<210> 378

<211> 205

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 378

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Met Ser Glu Ala Phe Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr
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Val Ala Leu Leu Asn Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala
                20                25                30

Leu Ser Ala Gly Ser Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu
                35                40                45

Glu Asp Thr Ser Ile Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro
                50                55                60

Leu Ala Arg Arg Ala Val Met Gly Lys Leu Met Ala Ile Val Ile Leu
                65                70                75                80

Ala Pro Ala Ala Phe Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala
                85                90                95

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Pro Gln Ala Pro Glu Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala
100 105 110

Val Val Ile Asn Gly Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln
115 120 125

His Gly Gly Ser Leu Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp
130 135 140

Val Leu Ile Asn Ile Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp
145 150 155 160

Thr Thr Ser Gly Trp Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu
165 170 175

Leu Ala Leu His Ala Ala His Glu Val Trp Glu Val Ser Glu Glu Glu
180 185 190

Arg Leu Ala Ser Lys Ala Leu Ala Gly Glu Ala Ile Asp
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<210> 379

<211> 1173

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1150)

<223> RXN00832

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ggaacggccc agagttctta agaaagtttg actagagAAC atg ccg ttt tct tgg 115
Met Pro Phe Ser Trp
1 5

cta aaa cca att gat tat gcc cgc atc ttt gtc ggc tgg gca tcg att 163
Leu Lys Pro Ile Asp Tyr Ala Arg Ile Phe Val Gly Trp Ala Ser Ile
10 15 20

ttt atc atc ccc ctc atc aca ctg cca tca att att gag ttg gcg ctg 211
Phe Ile Ile Pro Leu Ile Thr Leu Pro Ser Ile Ile Glu Leu Ala Leu
25 30 35

atc gtg gca gtc atc cta ttc tgc gca ttt ggc gtg gtg aag atg gcg 259
Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly Val Val Lys Met Ala
40 45 50

gag cgt ttg gct cat att ttg ggt gat cct ttt gga tcg ttg atc ctt 307
Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe Gly Ser Leu Ile Leu
55 60 65

acc ttg tcg atc gtg atc att gaa gtg att ttg atc tgt gcg gtg atg 355
Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu Ile Cys Ala Val Met
70 75 80 85

ctg ggg cct gct gat tca acc act gct ggt cgg gat tcc gtg atg gca 403

CCDS: C11732.1

Leu	Gly	Pro	Ala	Asp 90	Ser	Thr	Thr	Ala	Gly 95	Arg	Asp	Ser	Val	Met 100	Ala	
gtg Val	tcc Ser	atg Met	atc Ile 105	atc Ile	atg Met	ggg Gly	tgg Leu	gtc Val 110	gtg Val	gga Gly	tgg Leu	tgc Cys	cta Leu 115	ctc Leu	att Ile	451
ggg Gly	ggg Gly	tta Leu 120	agg Arg	cat His	gga Gly	agc Ser	atg Met 125	cca Pro	cac His	aat Asn	ggg Gly	gtg Val 130	gga Gly	act Thr	ccg Pro	499
acc Thr	tac Tyr 135	tgg Leu	gtg Val	ctg Leu	atc Ile	gca Ala 140	act Thr	ttt Phe	tcc Ser	gta Val	atc Ile 145	gcc Ala	ttt Phe	gcg Ala	gtt Val	547
cca Pro 150	gct Ala	ttc Phe	agg Arg	gga Gly	gaa Glu 155	tac Tyr	tcc Ser	act Thr	ggg Gly	cag Gln 160	gca Ala	ctt Leu	gtt Val	att Ile	tca Ser 165	595
aca Thr	ctg Leu	aca Thr	gca Ala	gtg Val 170	gtg Val	tac Tyr	ggg Gly	ttc Phe	ttc Phe 175	ctg Leu	ttt Phe	cgc Arg	caa Gln	atg Met 180	ggg Gly	643
gcc Ala	caa Gln	gct Ala	ggg Gly 185	gaa Glu	ttt Phe	caa Gln	gag Glu	gtc Val 190	gag Glu	gtc Val	gca Ala	gaa Glu	aag Lys 195	gca Ala	gac Asp	691
gac Asp	gca Ala	gca Ala 200	aaa Lys	tgg Trp	gag Glu	gtc Val	cca Pro 205	ttt Phe	aga Arg	ggc Gly	tta Leu	atc Ile 210	tgg Leu	att Ile	atc Ile	739
act Thr	gtg Val 215	ctc Leu	ccc Pro	atc Ile	gtg Val	tgg Leu 220	ctg Leu	tcc Ser	cat His	gac Asp	atg Met 225	gcc Ala	acg Thr	gtg Val	atg Met	787
gat Asp 230	gaa Glu	gtc Val	ctg Leu	gca Ala	agc Ser 235	ctt Leu	ggg Gly	gca Ala	ccc Pro	gta Val 240	gca Ala	atg Met	gct Ala	gga Gly	tta Leu 245	835
att Ile	att Ile	gcc Ala	acc Thr	att Ile 250	gtc Val	ttc Phe	tgg Leu	cca Pro	gag Glu 255	acc Thr	atc Ile	acc Thr	tcc Ser	tgg Leu 260	aaa Lys	883
gct Ala	gcg Ala	tgg Trp	aca Thr 265	gga Gly	gag Glu	att Ile	cag Gln	cga Arg 270	gta Val	agc Ser	aac Asn	ctc Leu	gcg Ala 275	cat His	gga Gly	931
gcc Ala	caa Gln	gta Val 280	tca Ser	acg Thr	gtg Val	ggg Gly	ctg Leu 285	aca Thr	atc Ile	cca Pro	gct Ala	gtt Val 290	cta Leu	gtg Val	atc Ile	979
ggc Gly	gtg Val 295	atc Ile	aca Thr	ggg Gly	caa Gln	gat Asp 300	gta Val	gtt Val	tgg Leu	ggg Gly	gag Glu 305	acc Thr	ccg Pro	atc Ile	aac Asn	1027
tgg Leu 310	tgg Leu	ctg Leu	ctg Leu	gga Gly	acc Thr 315	acc Thr	att Ile	gcg Ala	gtg Val	aca Thr 320	gcc Ala	att Ile	gcg Ala	ttt Phe	agc Ser 325	1075
tcc Ser	aag Lys	aaa Lys	gtc Val	agt Ser	gct Ala	gtg Val	cat His	ggc Gly	tgc Ser	gtg Val	ctg Leu	ctc Leu	atg Met	ctt Leu	ttc Phe	1123

330

335

340

ggt gtt tac atg atg agc atg ttc gcc tgatttaggt agcctggtgg
 Gly Val Tyr Met Met Ser Met Phe Ala
 345 350

1170

gaa

1173

<210> 380

<211> 350

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

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Gly Trp Ala Ser Ile Phe Ile Ile Pro Leu Ile Thr Leu Pro Ser Ile
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Ile Glu Leu Ala Leu Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly
 35 40 45

Val Val Lys Met Ala Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe
 50 55 60

Gly Ser Leu Ile Leu Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu
 65 70 75 80

Ile Cys Ala Val Met Leu Gly Pro Ala Asp Ser Thr Thr Ala Gly Arg
 85 90 95

Asp Ser Val Met Ala Val Ser Met Ile Ile Met Gly Leu Val Val Gly
 100 105 110

Leu Cys Leu Leu Ile Gly Gly Leu Arg His Gly Ser Met Pro His Asn
 115 120 125

Gly Val Gly Thr Pro Thr Tyr Leu Val Leu Ile Ala Thr Phe Ser Val
 130 135 140

Ile Ala Phe Ala Val Pro Ala Phe Arg Gly Glu Tyr Ser Thr Gly Gln
 145 150 155 160

Ala Leu Val Ile Ser Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu
 165 170 175

Phe Arg Gln Met Gly Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val
 180 185 190

Ala Glu Lys Ala Asp Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly
 195 200 205

Leu Ile Leu Ile Ile Thr Val Leu Pro Ile Val Leu Leu Ser His Asp
 210 215 220

Met Ala Thr Val Met Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val
 225 230 235 240

Ala Met Ala Gly Leu Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr

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<211> 578
<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA00832
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gcc	caa	gct	ggg	gaa	ttt	caa	gag	gtc	gag	gtc	gca	gaa	aag	gca	gac		96
Ala	Gln	Ala	Gly	Glu	Phe	Gln	Glu	Val	Glu	Val	Ala	Glu	Lys	Ala	Asp		
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gac	gca	gca	aaa	tgg	gag	gtc	cca	ttt	aga	ggc	tta	atc	ttg	att	atc		144
Asp	Ala	Ala	Lys	Trp	Glu	Val	Pro	Phe	Arg	Gly	Leu	Ile	Leu	Ile	Ile		
			35				40					45					
act	gtg	ctc	ccc	atc	gtg	ttg	ctg	tcc	cat	gac	atg	gcc	acg	gtg	atg		192
Thr	Val	Leu	Pro	Ile	Val	Leu	Leu	Ser	His	Asp	Met	Ala	Thr	Val	Met		
	50					55					60						
gat	gaa	gtc	ctg	gca	agc	ctt	ggg	gca	ccc	gta	gca	atg	gct	gga	tta		240
Asp	Glu	Val	Leu	Ala	Ser	Leu	Gly	Ala	Pro	Val	Ala	Met	Ala	Gly	Leu		
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att	att	gcc	acc	att	gtc	ttc	ttg	cca	gag	acc	atc	acc	tcc	ttg	aaa		288
Ile	Ile	Ala	Thr	Ile	Val	Phe	Leu	Pro	Glu	Thr	Ile	Thr	Ser	Leu	Lys		
				85					90					95			
gct	gcg	tgg	aca	gga	gag	att	cag	cga	gta	agc	aac	ctc	gcg	cat	gga		336
Ala	Ala	Trp	Thr	Gly	Glu	Ile	Gln	Arg	Val	Ser	Asn	Leu	Ala	His	Gly		
			100					105				110					
gcc	caa	gta	tca	acg	gtg	ggg	ctg	aca	atc	cca	gct	gtt	cta	gtg	atc		384

Ala	Gln	Val	Ser	Thr	Val	Gly	Leu	Thr	Ile	Pro	Ala	Val	Leu	Val	Ile	
	115						120				125					
ggc	gtg	atc	aca	ggg	caa	gat	gta	gtt	ttg	ggg	gag	acc	ccg	atc	aac	432
Gly	Val	Ile	Thr	Gly	Gln	Asp	Val	Val	Leu	Gly	Glu	Thr	Pro	Ile	Asn	
	130					135					140					
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Leu	Leu	Leu	Leu	Gly	Thr	Thr	Ile	Ala	Val	Thr	Ala	Ile	Ala	Phe	Ser	
145					150					155					160	
tcc	aag	aaa	gtc	agt	gct	gtg	cat	ggc	tcg	gtg	ctg	ctc	atg	ctt	ttc	528
Ser	Lys	Lys	Val	Ser	Ala	Val	His	Gly	Ser	Val	Leu	Leu	Met	Leu	Phe	
				165					170					175		
ggg	gtt	tac	atg	atg	agc	atg	ttc	gcc	tgatttaggt	agcctgggtgg						575
Gly	Val	Tyr	Met	Met	Ser	Met	Phe	Ala								
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gaa																578
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Asp	Ala	Ala	Lys	Trp	Glu	Val	Pro	Phe	Arg	Gly	Leu	Ile	Leu	Ile	Ile	
		35					40					45				
Thr	Val	Leu	Pro	Ile	Val	Leu	Leu	Ser	His	Asp	Met	Ala	Thr	Val	Met	
	50					55					60					
Asp	Glu	Val	Leu	Ala	Ser	Leu	Gly	Ala	Pro	Val	Ala	Met	Ala	Gly	Leu	
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Ile	Ile	Ala	Thr	Ile	Val	Phe	Leu	Pro	Glu	Thr	Ile	Thr	Ser	Leu	Lys	
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Ala	Ala	Trp	Thr	Gly	Glu	Ile	Gln	Arg	Val	Ser	Asn	Leu	Ala	His	Gly	
			100					105					110			
Ala	Gln	Val	Ser	Thr	Val	Gly	Leu	Thr	Ile	Pro	Ala	Val	Leu	Val	Ile	
	115						120					125				
Gly	Val	Ile	Thr	Gly	Gln	Asp	Val	Val	Leu	Gly	Glu	Thr	Pro	Ile	Asn	
	130					135					140					
Leu	Leu	Leu	Leu	Gly	Thr	Thr	Ile	Ala	Val	Thr	Ala	Ile	Ala	Phe	Ser	
145					150					155					160	
Ser	Lys	Lys	Val	Ser	Ala	Val	His	Gly	Ser	Val	Leu	Leu	Met	Leu	Phe	
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Gly Val Tyr Met Met Ser Met Phe Ala
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<210> 383
<211> 2733
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(2710)
<223> RXN00378

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Val Asp Lys Ala Val
1 5
aac act gct atc tct gac gcc aaa aca gcg gcg ctc aag gca ggt gtt 163
Asn Thr Ala Ile Ser Asp Ala Lys Thr Ala Ala Leu Lys Ala Gly Val
10 15 20
gga ttg aac cga gcc acc gcc tca gaa gaa gag gaa gat tta agc tca 211
Gly Leu Asn Arg Ala Thr Ala Ser Glu Glu Glu Glu Asp Leu Ser Ser
25 30 35
agc att aag gtt tct ttg gcc ttt gag ctc gag ggg tta agc aat gca 259
Ser Ile Lys Val Ser Leu Ala Phe Glu Leu Glu Gly Leu Ser Asn Ala
40 45 50
cca tcg ttg atg gtg gtg gaa aaa gcc cta gag aag atc ccc ggt gta 307
Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu Lys Ile Pro Gly Val
55 60 65
tcc gcg gat ctg att tac cct tca caa act gca tgg att aca gca act 355
Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala Trp Ile Thr Ala Thr
70 75 80 85
gat cgg gta cat ccc gaa acc ctc att gag gtg ttt gag cag ttc ggc 403
Asp Arg Val His Pro Glu Thr Leu Ile Glu Val Phe Glu Gln Phe Gly
90 95 100
atc aaa gca cac ctt tct aat tca tcg ctg ctg cgc agg cat caa cag 451
Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu Arg Arg His Gln Gln
105 110 115
ctc agc gcg gaa gta aat agg gaa gca cgc ctt gat cgt tac cgc tcc 499
Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu Asp Arg Tyr Arg Ser
120 125 130
cga atg gat gcc aag cga atc tcg cct cgt gtg cga agg cat aac cga 547
Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val Arg Arg His Asn Arg
135 140 145
caa gaa atg gta cat gcg gta cgc gct cgt gaa agt ggt tgg att aaa 595
Gln Glu Met Val His Ala Val Arg Ala Arg Glu Ser Gly Trp Ile Lys
150 155 160 165

cgc	agg	aat	cac	acc	acc	tcg	cag	cat	gaa	gac	cca	atg	tcg	ggc	gat	643
Arg	Arg	Asn	His	Thr	Thr	Ser	Gln	His	Glu	Asp	Pro	Met	Ser	Gly	Asp	
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gtg	ctg	ttc	acc	gcc	cgc	gca	ctg	att	aca	cct	aag	cgt	ttg	tgg	gtg	691
Val	Leu	Phe	Thr	Ala	Arg	Ala	Leu	Ile	Thr	Pro	Lys	Arg	Leu	Trp	Val	
				185					190					195		
tcg	ttg	ccg	ttt	gcg	ctc	atc	gta	ttg	gcg	tta	tcg	ttg	aat	cct	tcg	739
Ser	Leu	Pro	Phe	Ala	Leu	Ile	Val	Leu	Ala	Leu	Ser	Leu	Asn	Pro	Ser	
				200					205					210		
tgg	cag	ttt	gat	tat	tgg	cag	tgg	ttg	tcc	gct	gtg	ttg	gct	att	cct	787
Trp	Gln	Phe	Asp	Tyr	Trp	Gln	Trp	Leu	Ser	Ala	Val	Leu	Ala	Ile	Pro	
				215					220					225		
gtg	gtg	gtg	tgg	ggt	gcc	tgg	ccg	ttt	cac	cgc	gct	gca	gca	ggc	ggt	835
Val	Val	Val	Trp	Gly	Ala	Trp	Pro	Phe	His	Arg	Ala	Ala	Ala	Gly	Gly	
				230					235					240		
att	cgt	cga	gga	att	tcc	gct	ctt	gat	gcg	acc	agc	tca	atc	gct	att	883
Ile	Arg	Arg	Gly	Ile	Ser	Ala	Leu	Asp	Ala	Thr	Ser	Ser	Ile	Ala	Ile	
				250					255					260		
gct	gct	gca	tac	gcg	tgg	tct	atc	gcc	atg	ctg	ttg	ttt	gaa	acc	cca	931
Ala	Ala	Ala	Tyr	Ala	Trp	Ser	Ile	Ala	Met	Leu	Leu	Phe	Glu	Thr	Pro	
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gga	ggt	aaa	tcc	tgg	cgg	tca	tat	ccg	tcc	tgg	ttc	gct	ttt	gac	cac	979
Gly	Gly	Lys	Ser	Trp	Arg	Ser	Tyr	Pro	Ser	Trp	Phe	Ala	Phe	Asp	His	
				280					285					290		
ggc	acg	ttg	acc	caa	aac	gag	att	tat	ttt	gat	gtg	gcc	tgc	gga	atc	1027
Gly	Thr	Leu	Thr	Gln	Asn	Glu	Ile	Tyr	Phe	Asp	Val	Ala	Cys	Gly	Ile	
				295					300					305		
acc	gtg	ttg	ctt	ctt	gcc	gga	cgg	ctg	ctg	aca	agg	cgt	cga	agc	caa	1075
Thr	Val	Leu	Leu	Leu	Ala	Gly	Arg	Leu	Leu	Thr	Arg	Arg	Arg	Ser	Gln	
				310					315					320		
tcc	agt	ttg	tta	gcg	gaa	ctt	ggt	cgc	ctc	caa	atc	gat	cca	cag	cgc	1123
Ser	Ser	Leu	Leu	Ala	Glu	Leu	Gly	Arg	Leu	Gln	Ile	Asp	Pro	Gln	Arg	
				330					335					340		
att	gtc	act	gtg	gtg	cgt	aaa	cac	cga	ttg	aag	cgc	gta	gtc	cag	gaa	1171
Ile	Val	Thr	Val	Val	Arg	Lys	His	Arg	Leu	Lys	Arg	Val	Val	Gln	Glu	
				345					350					355		
ctg	aac	att	cca	gtg	cag	gaa	gtc	cgt	gtc	aat	gac	gat	gtg	aaa	gtt	1219
Leu	Asn	Ile	Pro	Val	Gln	Glu	Val	Arg	Val	Asn	Asp	Asp	Val	Lys	Val	
				360					365					370		
cca	cct	aat	acc	acg	atc	cct	gtg	gat	ggc	act	gtc	atc	ggt	ggc	ggt	1267
Pro	Pro	Asn	Thr	Thr	Ile	Pro	Val	Asp	Gly	Thr	Val	Ile	Gly	Gly	Gly	
				375					380					385		
tcg	cgg	atc	gca	gct	agc	atc	atc	atg	gga	caa	gac	cag	cgt	gat	gta	1315
Ser	Arg	Ile	Ala	Al												

Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu
 410 415 420
 atc aag gtt cgt gtt att cgc act ggt cac cgc acc cgc atc gcc gcg 1411
 Ile Lys Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala
 425 430 435
 gta cat agg tgg gtt aaa gaa gcg acg ttg aag gaa aac cgc cac aat 1459
 Val His Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn
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 agg gca gcg atc cgt tcg gcc ggt aac ctt gtg ccc atc acg ttc acc 1507
 Arg Ala Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr
 455 460 465
 ctt gct gtg gtg gac ttc tgt ctg tgg gca ctg atc tct gga aac atc 1555
 Leu Ala Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile
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 aac gct gca ttt acc act acc ttg gct gtc ctt gcg tgc gtg gct ccg 1603
 Asn Ala Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro
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 gtg gcc tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa 1651
 Val Ala Leu Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu
 505 510 515
 gct gca gca cga cac ggt att ttg gtc cgc tct ggt gaa att ttc cga 1699
 Ala Ala Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg
 520 525 530
 gtt ctc gat gat gtg gat act gcc gta ttt aat cgt gtg ggc aca cta 1747
 Val Leu Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu
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 acc gat ggc gaa atg aca gtg gaa acc gtc aca gca gac aaa ggc gag 1795
 Thr Asp Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu
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 Asp Pro Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser
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 cac cac gcg att tcc aaa gca ctg gtg aaa gca tcc cgt gaa gct cgt 1891
 His His Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg
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 gat acc ggc gcc ggt ggt gaa gat gtc cca cac tgg att gaa gta ggc 1939
 Asp Thr Gly Ala Gly Glu Asp Val Pro His Trp Ile Glu Val Gly
 600 605 610
 aac gtg gaa atc acc gaa gcc ggc tca ttc caa gca acc atc gag ctg 1987
 Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu
 615 620 625
 cca ctg atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca 2035
 Pro Leu Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala
 630 635 640 645
 ctc ctg tgg cga cca cga tcc atg aca gaa gtc cgt gag cac tta agc 2083
 Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser

GENE-TECH

650										655					660					
ccc	cga	cta	gtg	gca	gca	gca	acc	tca	ggt	ggc	gca	cca	ctg	atc	gtg	2131				
Pro	Arg	Leu	Val	Ala	Ala	Ala	Thr	Ser	Gly	Gly	Ala	Pro	Leu	Ile	Val					
665										670					675					
cga	tgg	aaa	ggc	aaa	gac	cgc	gga	gtt	atc	act	cta	agt	gac	cac	gtg	2179				
Arg	Trp	Lys	Gly	Lys	Asp	Arg	Gly	Val	Ile	Thr	Leu	Ser	Asp	His	Val					
680										685					690					
aga	tca	gat	tcc	tcc	gat	gcg	att	att	gcg	att	gaa	gaa	caa	ggc	atc	2227				
Arg	Ser	Asp	Ser	Ser	Asp	Ala	Ile	Ile	Ala	Ile	Glu	Glu	Gln	Gly	Ile					
695										700					705					
gag	acc	atg	atg	ctt	tca	cgt	gat	act	tac	ccg	gtg	gca	cgt	cga	tac	2275				
Glu	Thr	Met	Met	Leu	Ser	Arg	Asp	Thr	Tyr	Pro	Val	Ala	Arg	Arg	Tyr					
710										715					720					725
gca	gac	agc	tta	ggc	atc	acc	cac	gtc	ttg	gcc	ggc	atc	gcg	ccg	ggc	2323				
Ala	Asp	Ser	Leu	Gly	Ile	Thr	His	Val	Leu	Ala	Gly	Ile	Ala	Pro	Gly					
730										735					740					
aag	aaa	gcc	cag	gtc	gtc	cgt	gca	gtc	cac	acc	cgc	gga	tcc	act	gtc	2371				
Lys	Lys	Ala	Gln	Val	Val	Arg	Ala	Val	His	Thr	Arg	Gly	Ser	Thr	Val					
745										750					755					
gcg	atg	atc	ggc	gat	gaa	tca	gta	atg	gac	tgt	ttg	aaa	gtc	gct	gac	2419				
Ala	Met	Ile	Gly	Asp	Glu	Ser	Val	Met	Asp	Cys	Leu	Lys	Val	Ala	Asp					
760										765					770					
gtg	ggt	gta	ctg	atg	ggc	gtc	gat	cgt	ccc	tca	gat	ctg	cgt	gat	gat	2467				
Val	Gly	Val	Leu	Met	Gly	Val	Asp	Arg	Pro	Ser	Asp	Leu	Arg	Asp	Asp					
775										780					785					
tcc	gat	gac	ccg	gca	gct	gac	gtt	gtg	gtc	atg	cgc	gaa	gag	gtc	atg	2515				
Ser	Asp	Asp	Pro	Ala	Ala	Asp	Val	Val	Val	Met	Arg	Glu	Glu	Val	Met					
790										795					800					805
agc	gtg	ccg	acg	ctg	ttt	aaa	ctg	gct	cga	cgc	tac	gcc	aag	ttg	gtc	2563				
Ser	Val	Pro	Thr	Leu	Phe	Lys	Leu	Ala	Arg	Arg	Tyr	Ala	Lys	Leu	Val					
810										815					820					
aat	ggc	aat	att	gct	ctg	gcc	tgg	atc	tat	aac	ggt	gtt	gcc	atg	gtg	2611				
Asn	Gly	Asn	Ile	Ala	Leu	Ala	Trp	Ile	Tyr	Asn	Gly	Val	Ala	Met	Val					
825										830					835					
ctt	gca	gtg	tct	ggc	ttg	ctg	cat	cca	atg	gct	gcg	acc	gtg	gct	atg	2659				
Leu	Ala	Val	Ser	Gly	Leu	Leu	His	Pro	Met	Ala	Ala	Thr	Val	Ala	Met					
840										845					850					
ctg	gcg	tct	tcg	ctg	ctt	att	gaa	tgg	cgc	tcg	ggc	agg	gcg	cgc	aag	2707				
Leu	Ala	Ser	Ser	Leu	Leu	Ile	Glu	Trp	Arg	Ser	Gly	Arg	Ala	Arg	Lys					
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tac taaccagcaa ttcccaagcc caa															2733					
Tyr																				
870																				

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<211> 870

<213> Corynebacterium glutamicum

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Glu	Asp	Leu 35	Ser	Ser	Ser	Ile	Lys 40	Val	Ser	Leu	Ala	Phe 45	Glu	Leu	Glu
Gly	Leu 50	Ser	Asn	Ala	Pro	Ser 55	Leu	Met	Val	Val	Glu 60	Lys	Ala	Leu	Glu
Lys 65	Ile	Pro	Gly	Val	Ser 70	Ala	Asp	Leu	Ile	Tyr 75	Pro	Ser	Gln	Thr	Ala 80
Trp	Ile	Thr	Ala	Thr 85	Asp	Arg	Val	His	Pro 90	Glu	Thr	Leu	Ile	Glu 95	Val
Phe	Glu	Gln	Phe 100	Gly	Ile	Lys	Ala	His 105	Leu	Ser	Asn	Ser	Ser	Leu	Leu
Arg	Arg	His 115	Gln	Gln	Leu	Ser	Ala 120	Glu	Val	Asn	Arg	Glu 125	Ala	Arg	Leu
Asp	Arg 130	Tyr	Arg	Ser	Arg	Met 135	Asp	Ala	Lys	Arg	Ile 140	Ser	Pro	Arg	Val
Arg 145	Arg	His	Asn	Arg	Gln 150	Glu	Met	Val	His	Ala 155	Val	Arg	Ala	Arg	Glu 160
Ser	Gly	Trp	Ile 165	Lys	Arg	Arg	Asn	His	Thr 170	Thr	Ser	Gln	His	Glu 175	Asp
Pro	Met	Ser	Gly 180	Asp	Val	Leu	Phe	Thr 185	Ala	Arg	Ala	Leu	Ile 190	Thr	Pro
Lys	Arg	Leu 195	Trp	Val	Ser	Leu	Pro 200	Phe	Ala	Leu	Ile	Val 205	Leu	Ala	Leu
Ser	Leu 210	Asn	Pro	Ser	Trp	Gln 215	Phe	Asp	Tyr	Trp	Gln 220	Trp	Leu	Ser	Ala
Val 225	Leu	Ala	Ile	Pro	Val 230	Val	Val	Trp	Gly	Ala 235	Trp	Pro	Phe	His	Arg 240
Ala	Ala	Ala	Gly 245	Gly	Ile	Arg	Arg	Gly	Ile 250	Ser	Ala	Leu	Asp	Ala 255	Thr
Ser	Ser	Ile 260	Ala	Ile	Ala	Ala	Ala	Tyr 265	Ala	Trp	Ser	Ile	Ala 270	Met	Leu
Leu	Phe	Glu 275	Thr	Pro	Gly	Gly	Lys 280	Ser	Trp	Arg	Ser	Tyr 285	Pro	Ser	Trp
Phe 290	Ala	Phe	Asp	His	Gly 295	Thr	Leu	Thr	Gln	Asn	Glu 300	Ile	Tyr	Phe	Asp

Category	Item	Value
General Information	Project Name	Project A
	Project ID	12345
	Project Manager	John Doe
	Project Status	In Progress
	Project Start Date	2023-01-01
	Project End Date	2023-12-31
	Project Budget	\$1,000,000
	Project Location	New York, NY
	Project Team	10 members
	Project Description	A new software application for managing project resources.
Financial Data	Revenue	\$500,000
	Costs	\$300,000
	Profit	\$200,000
	Net Income	\$150,000
	Operating Expenses	\$180,000
	Capital Expenses	\$120,000
	Depreciation	\$60,000
	Interest	\$40,000
	Taxes	\$30,000
	Dividends	\$20,000
Operational Data	Production Volume	10,000 units
	Quality Score	95%
	Customer Satisfaction	4.5/5
	Employee Turnover	5%
	Inventory Levels	1,000 units
	Supply Chain Efficiency	90%
	Logistics Cost	\$50,000
	Marketing Spend	\$20,000
	R&D Spend	\$30,000
	IT Spend	\$10,000
Human Resources	Headcount	50 employees
	Recruitment	10 new hires
	Training	500 hours
	Performance	85% average
	Retention	90%
	Compensation	\$1,200,000
	Benefits	\$200,000
	Healthcare	\$50,000
	Disability	\$20,000
	Life Insurance	\$10,000

625 630 635 640
 Arg Thr Thr Glu Ala Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val
 645 650 655
 Arg Glu His Leu Ser Pro Arg Leu Val Ala Ala Ala Thr Ser Gly Gly
 660 665 670
 Ala Pro Leu Ile Val Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr
 675 680 685
 Leu Ser Asp His Val Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile
 690 695 700
 Glu Glu Gln Gly Ile Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro
 705 710 715 720
 Val Ala Arg Arg Tyr Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala
 725 730 735
 Gly Ile Ala Pro Gly Lys Lys Ala Gln Val Val Arg Ala Val His Thr
 740 745 750
 Arg Gly Ser Thr Val Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys
 755 760 765
 Leu Lys Val Ala Asp Val Gly Val Leu Met Gly Val Asp Arg Pro Ser
 770 775 780
 Asp Leu Arg Asp Asp Ser Asp Asp Pro Ala Ala Asp Val Val Val Met
 785 790 795 800
 Arg Glu Glu Val Met Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg
 805 810 815
 Tyr Ala Lys Leu Val Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn
 820 825 830
 Gly Val Ala Met Val Leu Ala Val Ser Gly Leu Leu His Pro Met Ala
 835 840 845
 Ala Thr Val Ala Met Leu Ala Ser Ser Leu Leu Ile Glu Trp Arg Ser
 850 855 860
 Gly Arg Ala Arg Lys Tyr
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<211> 1796

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1773)

<223> FRXA00378

<400> 385

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 Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His Gly Thr

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ttg acc caa aac gag att tat ttt gat gtg gcc tgc gga atc acc gtg				96
Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile Thr Val	20	25	30	
ttg ctt ctt gcc gga cgg ctg ctg aca agg cgt cga agc caa tcc agt				144
Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln Ser Ser	35	40	45	
ttg tta gcg gaa ctt ggt cgc ctc caa atc gat cca cag cgc att gtc				192
Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg Ile Val	50	55	60	
act gtg gtg cgt aaa cac cga ttg aag cgc gta gtc cag gaa ctg aac				240
Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu Leu Asn	65	70	75	80
att cca gtg cag gaa gtc cgt gtc aat gac gat gtg aaa gtt cca cct				288
Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val Pro Pro	85	90	95	
aat acc acg atc cct gtg gat ggc act gtc atc ggt ggc ggt tcc cgg				336
Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Ser Arg	100	105	110	
atc gca gct agc atc atc atg gga caa gac cag cgt gat gta aaa gta				384
Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val Lys Val	115	120	125	
aat gac aaa gtt ttc gcc ggc agc ctc aac ctc gaa tcc gaa atc aag				432
Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu Ile Lys	130	135	140	
gtt cgt gtt att cgc act ggt cac cgc acc cgc atc gcc gcg gta cat				480
Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His	145	150	155	160
agg tgg gtt aaa gaa gcg acg ttg aag gaa aac cgc cac aat agg gca				528
Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn Arg Ala	165	170	175	
gcg atc cgt tcc gcc ggt aac ctt gtg ccc atc acg ttc acc ctt gct				576
Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr Leu Ala	180	185	190	
gtg gtg gac ttc tgt ctg tgg gca ctg atc tct gga aac atc aac gct				624
Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile Asn Ala	195	200	205	
gca ttt acc act acc ttg gct gtc ctt gcg tgc gtg gct ccg gtg gcc				672
Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro Val Ala	210	215	220	
tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa gct gca				720
Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu Ala Ala	225	230	235	240
gca cga cac ggt att ttg gtc cgc tct ggt gaa att ttc cga gtt ctc				768
Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg Val Leu	245	250	255	

gat gat gtg gat act gcc gta ttt aat cgt gtg ggc aca cta acc gat 816
Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu Thr Asp
260 265 270

ggc gaa atg aca gtg gaa acc gtc aca gca gac aaa ggc gag gac cca 864
Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu Asp Pro
275 280 285

gaa cta gtg ctg cgt gtc gcc ggg gcg ttg gcc atg gaa tcc cac cac 912
Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser His His
290 295 300

gcg att tcc aaa gca ctg gtg aaa gca tcc cgt gaa gct cgt gat acc 960
Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg Asp Thr
305 310 315 320

ggc gcc ggt ggt gaa gat gtc cca cac tgg att gaa gta ggc aac gtg 1008
Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly Asn Val
325 330 335

gaa atc acc gaa gcc ggc tca ttc caa gca acc atc gag ctg cca ctg 1056
Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu Pro Leu
340 345 350

atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca ctc ctg 1104
Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala Leu Leu
355 360 365

tgg cga cca cga tcc atg aca gaa gtc cgt gag cac tta agc ccc cga 1152
Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser Pro Arg
370 375 380

cta gtg gca gca gca acc tca ggt ggc gca cca ctg atc gtg cga tgg 1200
Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val Arg Trp
385 390 395 400

aaa ggc aaa gac cgc gga gtt atc act cta agt gac cac gtg aga tca 1248
Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val Arg Ser
405 410 415

gat tcc tcc gat gcg att att gcg att gaa gaa caa ggc atc gag acc 1296
Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile Glu Thr
420 425 430

atg atg ctt tca cgt gat act tac ccg gtg gca cgt cga tac gca gac 1344
Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr Ala Asp
435 440 445

agc tta ggc atc acc cac gtc ttg gcc ggc atc gcg ccg ggc aag aaa 1392
Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly Lys Lys
450 455 460

gcc cag gtc gtc cgt gca gtc cac acc cgc gga tcc act gtc gcg atg 1440
Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val Ala Met
465 470 475 480

atc ggc gat gaa tca gta atg gac tgt ttg aaa gtc gct gac gtg ggt 1488
Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp Val Gly
485 490 495

Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	15.2	5.8	10	25
Health status	0.7	0.4	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.4	0.5	0	1
Stress level	0.6	0.5	0	1
Sleep quality	0.5	0.5	0	1
Dietary habits	0.4	0.5	0	1
Work-life balance	0.3	0.5	0	1
Family support	0.6	0.5	0	1
Community involvement	0.4	0.5	0	1
Overall well-being	0.5	0.5	0	1

145		150		155		160
Arg Trp Val Lys	Glu Ala Thr Leu Lys	Glu Asn Arg His Asn Arg Ala				
	165	170			175	
Ala Ile Arg Ser	Ala Gly Asn Leu Val	Pro Ile Thr Phe Thr Leu Ala				
	180	185			190	
Val Val Asp Phe	Cys Leu Trp Ala Leu Ile Ser	Gly Asn Ile Asn Ala				
	195	200			205	
Ala Phe Thr Thr	Thr Leu Ala Val Leu Ala Cys	Val Ala Pro Val Ala				
	210	215			220	
Leu Ala Leu Ser	Ala Pro Leu Ala Thr Arg	Asn Ser Ile Glu Ala Ala				
	225	230			235	240
Ala Arg His Gly	Ile Leu Val Arg Ser Gly	Glu Ile Phe Arg Val Leu				
	245	250			255	
Asp Asp Val Asp	Thr Ala Val Phe Asn Arg	Val Gly Thr Leu Thr Asp				
	260	265			270	
Gly Glu Met Thr	Val Glu Thr Val Thr Ala	Asp Lys Gly Glu Asp Pro				
	275	280			285	
Glu Leu Val Leu	Arg Val Ala Gly Ala Leu	Ala Met Glu Ser His His				
	290	295			300	
Ala Ile Ser Lys	Ala Leu Val Lys Ala Ser	Arg Glu Ala Arg Asp Thr				
	305	310			315	320
Gly Ala Gly Gly	Glu Asp Val Pro His Trp	Ile Glu Val Gly Asn Val				
	325	330			335	
Glu Ile Thr Glu	Ala Gly Ser Phe Gln Ala	Thr Ile Glu Leu Pro Leu				
	340	345			350	
Ile Lys Pro Ser	Gly Glu Lys Ile Met Arg	Thr Thr Glu Ala Leu Leu				
	355	360			365	
Trp Arg Pro Arg	Ser Met Thr Glu Val Arg	Glu His Leu Ser Pro Arg				
	370	375			380	
Leu Val Ala Ala	Ala Thr Ser Gly Gly Ala	Pro Leu Ile Val Arg Trp				
	385	390			395	400
Lys Gly Lys Asp	Arg Gly Val Ile Thr Leu	Ser Asp His Val Arg Ser				
	405	410			415	
Asp Ser Ser Asp	Ala Ile Ile Ala Ile Glu	Glu Gln Gly Ile Glu Thr				
	420	425			430	
Met Met Leu Ser	Arg Asp Thr Tyr Pro Val	Ala Arg Arg Tyr Ala Asp				
	435	440			445	
Ser Leu Gly Ile	Thr His Val Leu Ala Gly	Ile Ala Pro Gly Lys Lys				
	450	455			460	
Ala Gln Val Val	Arg Ala Val His Thr Arg	Gly Ser Thr Val Ala Met				
	465	470			475	480

Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp Val Gly
 485 490 495

Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp Ser Asp
 500 505 510

Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met Ser Val
 515 520 525

Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val Asn Gly
 530 535 540

Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val Leu Ala
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Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met Leu Ala
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 Leu Ser Thr Lys Asn
 1 5

tac cac gtc gag ggt ttg acc tgc gca aac ggt gta gct tcc gta gag 163
 Tyr His Val Glu Gly Leu Thr Cys Ala Asn Gly Val Ala Ser Val Glu
 10 15 20

gat gaa atc ggc att gtt gcg ggc acc cag ggt gtg gat att gat att 211
 Asp Glu Ile Gly Ile Val Ala Gly Thr Gln Gly Val Asp Ile Asp Ile
 25 30 35

gag acc ggc cgc gtc acg gtg act ggt gaa ggt ttc act gac gag gaa 259
 Glu Thr Gly Arg Val Thr Val Thr Gly Glu Gly Phe Thr Asp Glu Glu
 40 45 50

atc att gag gct gtc gcg aac gcg ggc tac aaa gtt tct ggg cgg 304
 Ile Ile Glu Ala Val Ala Asn Ala Gly Tyr Lys Val Ser Gly Arg
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tagcacaatt acacattcat etc 327

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<213> Corynebacterium glutamicum

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Val Ser Gly Arg
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<210> 389

<211> 1925

<212> DNA

<213> Corynebacterium glutamicum

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<222> (1) . . (1902)

<223> RXN01338

<400> 389

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ggc atc atc act gtc gca gcc ctt gtt gcc atc gca ata cat ctc att 96
Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile His Leu Ile
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tta	tgg	ctg	gct	cta	gat	cta	gat	ggc	ctt	gct	aaa	aac	tgg	cct	tta	144
Leu	Trp	Leu	Ala	Leu	Asp	Leu	Asp	Gly	Leu	Ala	Lys	Asn	Trp	Pro	Leu	
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aaa tca gcc att aaa act cgc ggt ggc gcg gat act tta gca gca gtc 240
Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val
65 70 75 80

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Ser	Ile	Ile	Thr	Ser	Val	Leu	Leu	Gly	Glu	Trp	Leu	Val	Ala	Ala	Ile	
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atc gtg ctc atg ctc tct ggt ggt gaa gcg cta gaa gag gca gca tca 336
Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser
100 105 110

cgg cga gcc agt ggc acc ttg gac gca ctt gcc cgg cgc gca cca agt 384
Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser

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cat gaa ctt tgt ccc gtg gat ggt gaa atc gtg gca ggc cac ggc acc His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr 165 170 175			528
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acg att gtt gcc aca aag ctt gcc cat gat tcc aga tac gcc caa att Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile 210 215 220			672
gtt ggt gta ctc cat gaa gca gaa aac aac cgc cca gaa atg cgc agg Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg 225 230 235 240			720
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gcg atc atc ggt gcg att tct ctt gcg gct cgt cgg ggc atc atc gtg Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly Ile Ile Val 290 295 300			912
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gct tca gta gag cgc tac tcc aga cac ccg ttg gct gac gcg att cgt Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg 355 360 365			1104

G E S S - T H E G E S S

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tcg gaa cgt cca gga cag gga cta acc ggc acg gtg ggc gag cac ctg 1200
 Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu
 385 390 395 400

gtt cga ata acc aat agg cgc agc aca cta gaa att gat cca gac agc 1248
 Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser
 405 410 415

aag aac tac att ccg gtg aca agt tcc ggc atg gaa tct gtg gtg ctt 1296
 Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu
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gtt gat gat aaa tat gca gca ctc att cgc ctc cgg gat gaa cct cgt 1344
 Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg
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 Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val
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gac aag ctc atg att atc tct ggt gat cgc gca tct gag gtt cgt tac 1440
 Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr
 465 470 475 480

ctt gcg gac aag gtt ggc att gat gag gta cac gca gag gcc tca ccg 1488
 Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro
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gaa gac aag ctg aac att gtt aat cgg cat aat gag cac ggc gcc acc 1536
 Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr
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atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg gcc gtt gcc 1584
 Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala
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acc gtt ggt gtc gcg atg gga gca gac tcc gat gtc acg tcc gaa gca 1632
 Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala
 530 535 540

gca gat gct gtg att ttg gat tct tcc ctg gaa cgt ctc gac gat ctg 1680
 Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu
 545 550 555 560

ctc cac atc agt gca cgg atg cgt cga ata gcg ttg caa tct gcg ggc 1728
 Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly
 565 570 575

ggt ggc atg gcg ttg agt gtc ata gga atg atc ctc gcg gta ttt gga 1776
 Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly
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ttc ttg acg cca ctg atg ggt gcg atc ttc caa gag gtc att gac gtg 1824
 Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val Ile Asp Val
 595 600 605

ctg gct atc ctc aat tcc gct cgg gtc gca ctg cca cgc gga gcg att 1872
 Leu Ala Ile Leu Asn Ser Ala Arg Val Ala Leu Pro Arg Gly Ala Ile
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cgt 1925

<210> 390

<211> 634

<212> PRT

<213> *Corynebacterium glutamicum*

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Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu
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Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu
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Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val
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Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile
 85 90 95

Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser
 100 105 110

Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser
 115 120 125

Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly Thr Glu Glu
 130 135 140

Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala Val Leu Pro
 145 150 155 160

His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr
 165 170 175

Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val Ser Lys Ser
 180 185 190

Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp Thr Pro Leu
 195 200 205

Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile
 210 215 220

Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg
 225 230 235 240

Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala Leu Ala Leu
 245 250 255
 Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg Phe Leu Ala
 260 265 270
 Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala Val Pro Val
 275 280 285
 Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly Ile Ile Val
 290 295 300
 Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys Thr Val Met
 305 310 315 320
 Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val Ile Thr Asp
 325 330 335
 Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu Ala Leu Ala
 340 345 350
 Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg
 355 360 365
 Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val Val Glu Val
 370 375 380
 Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu
 385 390 395 400
 Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser
 405 410 415
 Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu
 420 425 430
 Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg
 435 440 445
 Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val
 450 455 460
 Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr
 465 470 475 480
 Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro
 485 490 495
 Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr
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 Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala
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<211> 2001
<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA01338
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Met Leu Phe Ile Arg																115
1 5																
tca ttt gat ggc atc atc act gtc gca gcc ctt gtt gcc atc gca ata																163
Ser Phe Asp Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile																
10 15 20																
cat ctc att tta tgg ctg gct cta gat cta gat ggc ctt gct aaa aac																211
His Leu Ile Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn																
25 30 35																
tgg cct tta ata gcc atc gtt atc gta ggt ggc att ccg ttg atg tgg																259
Trp Pro Leu Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp																
40 45 50																
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Asp Val Leu Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu																
55 60 65																
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Ala Ala Ile Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu																
90 95 100																
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Ala Ala Ser Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg																
105 110 115																

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Ala Pro Ser Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly	
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Thr Glu Glu Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala	
135 140 145	
gtg ctc ccg cat gaa ctt tgt ccc gtg gat ggt gaa atc gtg gca ggc	595
Val Leu Pro His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly	
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His Gly Thr Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val	
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Ser Lys Ser Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp	
185 190 195	
act ccg ctg acg att gtt gcc aca aag ctt gcc cat gat tcc aga tac	739
Thr Pro Leu Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr	
200 205 210	
gcc caa att gtt ggt gta ctc cat gaa gca gaa aac aac cgc cca gaa	787
Ala Gln Ile Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu	
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Met Arg Arg Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala	
230 235 240 245	
ctt gcc ctc ggt ggt ctt ggc tgg att gtc tcc ggc gac cca gtg agg	883
Leu Ala Leu Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg	
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Phe Leu Ala Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala	
265 270 275	
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Val Pro Val Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly	
280 285 290	
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Ile Thr Asp Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu	
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Ala Leu Ala Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp	
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Ala Ile Arg Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val	
360 365 370	
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Val Glu Val Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly	
375 380 385	
gag cac ctg gtt cga ata acc aat agg cgc agc aca cta gaa att gat	1315
Glu His Leu Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp	
390 395 400 405	
cca gac agc aag aac tac att ccg gtg aca agt tcc ggc atg gaa tct	1363
Pro Asp Ser Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser	
410 415 420	
gtg gtg ctt gtt gat gat aaa tat gca gca ctc att cgc ctc cgg gat	1411
Val Val Leu Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp	
425 430 435	
gaa cct cgt gca tct gcc agt gag ttc atc gcg cac ttg ccc aag aag	1459
Glu Pro Arg Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys	
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cac aaa gtg gac aag ctc atg att atc tct ggt gat cgc gca tct gag	1507
His Lys Val Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu	
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gtt cgt tac ctt gcg gac aag gtt ggc att gat gag gta cac gca gag	1555
Val Arg Tyr Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu	
470 475 480 485	
gcc tca ccg gaa gac aag ctg aac att gtt aat ccg cat aat gag cac	1603
Ala Ser Pro Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His	
490 495 500	
ggc gcc acc atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg	1651
Gly Ala Thr Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met	
505 510 515	
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Ala Val Ala Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr	
520 525 530	
tcc gaa gca gca gat gct gtg att ttg gat tct tcc ctg gaa cgt ctc	1747
Ser Glu Ala Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu	
535 540 545	
gac gat ctg ctc cac atc agt gca cgg atg cgt cga ata gcg ttg caa	1795
Asp Asp Leu Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln	
550 555 560 565	
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Ser Ala Gly Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala	
570 575 580	
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Val Phe Gly Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val	
585 590 595	
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Ile Asp Val Leu Ala Ile Leu Asn Ser Ala Arg Val Ala Leu Pro Arg	

600 605 610
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acctaaatgt cgt 2001

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 35 40 45
 Ile Pro Leu Met Trp Asp Val Leu Lys Ser Ala Ile Lys Thr Arg Gly
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 Gly Ala Asp Thr Leu Ala Ala Val Ser Ile Ile Thr Ser Val Leu Leu
 65 70 75 80
 Gly Glu Trp Leu Val Ala Ala Ile Ile Val Leu Met Leu Ser Gly Gly
 85 90 95
 Glu Ala Leu Glu Glu Ala Ala Ser Arg Arg Ala Ser Gly Thr Leu Asp
 100 105 110
 Ala Leu Ala Arg Arg Ala Pro Ser Thr Ala His Arg Leu Leu Gly Ala
 115 120 125
 Thr Ile Leu Asp Gly Thr Glu Glu Ile Ala Val Glu Glu Ile Thr Val
 130 135 140
 Gly Asp Leu Val Ala Val Leu Pro His Glu Leu Cys Pro Val Asp Gly
 145 150 155 160
 Glu Ile Val Ala Gly His Gly Thr Met Asp Glu Ser Tyr Leu Thr Gly
 165 170 175
 Glu Pro Tyr Val Val Ser Lys Ser Lys Gly Ser Gln Ala Met Ser Gly
 180 185 190
 Ala Val Asn Gly Asp Thr Pro Leu Thr Ile Val Ala Thr Lys Leu Ala
 195 200 205
 His Asp Ser Arg Tyr Ala Gln Ile Val Gly Val Leu His Glu Ala Glu
 210 215 220
 Asn Asn Arg Pro Glu Met Arg Arg Met Ala Asp Arg Leu Gly Ala Trp
 225 230 235 240
 Tyr Thr Val Ile Ala Leu Ala Leu Gly Gly Leu Gly Trp Ile Val Ser

245										250					255				
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	290					295					300								
Ala	Ser	Gly	Val	Lys	Thr	Val	Met	Phe	Asp	Lys	Thr	Gly	Thr	Leu	Thr				
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Tyr	Gly	Arg	Pro	Val	Ile	Thr	Asp	Ile	His	Thr	Ala	Pro	Gly	Val	Glu				
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Glu	Asp	Thr	Val	Leu	Ala	Leu	Ala	Ala	Ser	Val	Glu	Arg	Tyr	Ser	Arg				
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His	Pro	Leu	Ala	Asp	Ala	Ile	Arg	Glu	Gly	Ala	Lys	Ala	Arg	Glu	Leu				
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His	Leu	Pro	Asp	Val	Val	Glu	Val	Ser	Glu	Arg	Pro	Gly	Gln	Gly	Leu				
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Ser	Gly	Met	Glu	Ser	Val	Val	Leu	Val	Asp	Asp	Lys	Tyr	Ala	Ala	Leu				
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Ile	Arg	Leu	Arg	Asp	Glu	Pro	Arg	Ala	Ser	Ala	Ser	Glu	Phe	Ile	Ala				
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Asp	Arg	Ala	Ser	Glu	Val	Arg	Tyr	Leu	Ala	Asp	Lys	Val	Gly	Ile	Asp				
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Arg	His	Asn	Glu	His	Gly	Ala	Thr	Met	Phe	Leu	Gly	Asp	Gly	Ile	Asn				
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Ser	Leu	Glu	Arg	Leu	Asp	Asp	Leu	Leu	His	Ile	Ser	Ala	Arg	Met	Arg				
545					550					555					560				
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His	Trp	Thr	Asp	Thr	Ile	Val	Ile	Gly	Ala	Val	Val	Ile	Ile	Asn	Met		
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Met	Val	Gly	Phe	Ile	Gln	Glu	Gly	Lys	Ala	Ala	Asp	Ala	Leu	Ala	Ser		
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Ile	Arg	Asn	Met	Leu	Ser	Pro	Glu	Ser	Ala	Ala	Leu	Arg	Asp	Gly	Val		
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 Thr Asn Leu His Ile Glu Glu Ser Ala Leu Thr Gly Glu Ala Glu Ala
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Ile Val Leu Ala Asp Asp Asn Phe Ala Thr Ile Ala Gly Ala Val Glu	
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Ile Asp Ala Pro Ser Val Leu Arg Ile Val Tyr Val Ser Leu Leu Leu	
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Pro Ile Ala Gln Ser Ala Tyr Gln Ala Leu Arg Ile Arg Met Val Ser
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Ile Asp Leu Leu Val Val Val Ala Ala Val Gly Ala Met Phe Ile Asn
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Asn Tyr Trp Glu Ser Ala Ala Val Thr Phe Leu Phe Ala Leu Gly Lys
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Ala Leu Glu Arg Ala Thr Met Asn Arg Thr Arg Lys Ala Leu Ser Asp
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Leu Val Asp Ala Ala Pro Glu Thr Ala Thr Arg Leu Asn Ala Asp Asp
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Ser Thr Glu Val Val Glu Leu Trp Glu Leu Glu Pro Gly Asp Ile Val
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Leu Val Arg Asn Gly Glu Gln Ile Pro Val Asp Gly Asn Val Ile Ala
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Gly Val Gly Gly Ile Asp Glu Ser Asn Ile Thr Gly Glu Ser Met Pro
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Ala Glu Lys Gly Gln Gly Ser Asp Val Tyr Ala Gly Thr Trp Leu Arg
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Ser Gly Val Leu Arg Val Glu Ala Thr Gly Ile Gly Ser Asp Ser Thr
165 170 175

Leu Ala Lys Ile Ile His Arg Val Glu Asp Ala Gln Asp Asp Lys Ala
180 185 190

Arg Thr Gln Thr Phe Leu Glu Lys Phe Ser Lys Trp Tyr Thr Pro Gly
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Val Met Ile Ala Ala Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu
210 215 220

Leu Ala Leu Thr Leu Leu Val Ile Gly Cys Pro Gly Ala Leu Val Ile
225 230 235 240

Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp
245 250 255

Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val
260 265 270

Asp Val Val Val Val Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro
275 280 285

Glu Leu Thr Asp Val Glu Val Ile Glu Pro Ala Tyr Ser Gln Gly Glu
290 295 300

Val Leu Glu Leu Ala Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu
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Ala Asp Ala Ile Ile Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr
325 330 335

Leu Val Glu Ala Ala Glu Asn Ile Thr Gly Arg Gly Ile Ile Ala Asn
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Val Asp Gly Gln Ala Val Ala Val Gly Ser Ala Glu Leu Leu Asp His

U E S - T E C H N I C A L

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Lys	Ala	Gly	Ile	Gln	Val	Val	Met	Ala	Thr	Gly	Asp	Ala	His	Arg	Val
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Ala	Gln	Asn	Val	Ala	Ser	Lys	Leu	Gly	Val	Asp	Glu	Val	Tyr	Ser	Glu
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Arg	Ile	Asn	Ile	Leu	Ile	Ala	Leu	Ala	Thr	Val	Met	Val	Leu	Leu	Ala
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Gly	Val	Leu	Phe	Gly	Gly	Val	Thr	Met	Ser	Val	Gly	Met	Leu	Val	His
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Glu	Ala	Ser	Val	Leu	Leu	Val	Ile	Ser	Ile	Ala	Met	Leu	Leu	Leu	Arg
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Pro	Thr	Leu	Lys	Glu	Asp	Ala	Ala	Gln	Ala	Ser	Asp	Ile	Lys	Arg	Ser
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<211> 762

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<213> Corynebacterium glutamicum

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Met Phe Val Gly Val
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Asn Gly His Ala Ile Gly Ile Val Ala Val Ala Asp Ala Val Arg Ser
10 15 20

gat tct gcc tca gca atc gaa tcg ctg cat aag gcg ggc att caa gtt 211
Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys Ala Gly Ile Gln Val
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gtc atg gcg act ggc gac gct cac cgc gtt gca caa aac gtg gcc tcc 259
Val Met Ala Thr Gly Asp Ala His Arg Val Ala Gln Asn Val Ala Ser
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Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu Leu Pro Glu Gln Lys
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Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu Ala Ala Ala Asp Ile
90 95 100

gga gta gcg atg ggc gtg gca ggt tcc cct gca gcc att gaa acc gct 451
Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala Ala Ile Glu Thr Ala
105 110 115

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Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg Leu Ala His Ala Val
120 125 130

acc ttg gca aaa cgc acc gta aga acc atg cgc atc aat att ctg att 547
Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg Ile Asn Ile Leu Ile
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gcg ttg gct acc gtg atg gtg tta cta gct ggc gtc cta ttt ggc gga 595
Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly Val Leu Phe Gly Gly
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Val Thr Met Ser Val Gly Met Leu Val His Glu Ala Ser Val Leu Leu
170 175 180

gtt atc agc atc gcc atg ctg ttg ctg cgt cca aca ctt aaa gaa gat 691
Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro Thr Leu Lys Glu Asp
185 190 195

gct gcg caa gca agt gat att aaa cgc tcg gaa ata caa cag atc gca 739
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<213> Corynebacterium glutamicum

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35 40 45

Gln Asn Val Ala Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu
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Leu Pro Glu Gln Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly
65 70 75 80

Lys Thr Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu
85 90 95

Ala Ala Ala Asp Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala
100 105 110

Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg
115 120 125

Leu Ala His Ala Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg
130 135 140

Ile Asn Ile Leu Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly
145 150 155 160

Val Leu Phe Gly Gly Val Thr Met Ser Val Gly Met Leu Val His Glu
165 170 175

Ala Ser Val Leu Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro
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<211> 2007

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<222> (101) .. (1984)

<223> RXN02348

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aaa Lys	agt Ser	gcg Ala	cgg Arg	cca Pro 10	aaa Lys	tca Ser	gtc Val	gct Ala	cca Pro 15	aaa Lys	tcc Ser	gga Gly	caa Gln 20	gct Ala	tta Leu	163
ctc Leu	act Thr	ctc Leu	ggg Gly 25	gcc Ala	cta Leu	ggt Gly	gtt Val	gtg Val 30	ttc Phe	ggc Gly	gac Asp	atc Ile	ggc Gly 35	acc Thr	agc Ser	211
ccc Pro	ctg Leu	tac Tyr 40	tca Ser	ctt Leu	cac His	act Thr	gca Ala 45	ttc Phe	agc Ser	atg Met	cag Gln 50	cac His	aac Asn	aaa Lys	gtc Val	259
gaa Glu	gtc Val 55	act Thr	cag Gln	gaa Glu	aat Asn	gtg Val 60	tac Tyr	ggc Gly	atc Ile	atc Ile	tcc Ser 65	atg Met	gtg Val	ttg Leu	tgg Trp	307
acc Thr 70	atc Ile	act Thr	ttg Leu	atc Ile 75	gtc Val 75	acc Thr	gtc Val	aaa Lys	tac Tyr 80	gtc Val	atg Met	ctg Leu	gtc Val	acc Thr 85	cga Arg 85	355
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atg Met	ttg Leu	ctg Leu	tgg Trp 185	ttt Phe	gtc Val	acc Thr	ctt Leu	gca Ala 190	gga Gly	ttg Leu	gga Gly	att Ile	ccg Pro 195	caa Gln	atc Ile	691
atc Ile	ggg Gly 200	cac His	cca Pro	gaa Glu	atc Ile	ttg Leu	cag Gln 205	agc Ser	ttg Leu	tct Ser	cca Pro 210	cat His	tgg Trp	gcc Ala	ctg Leu	739
cgc Arg 215	ttg Leu	att Ile	gtg Val	gct Ala	gag Glu	cct Pro 220	ttc Phe	caa Gln	gca Ala	ttt Phe	gtg Val 225	ctg Leu	ctt Leu	ggt Gly	gcc Ala	787
gtt Val	gtc Val	ctg Leu	aca Thr	gta Val	acg Thr	ggg Gly	gcg Ala	gaa Glu	gcg Ala	ctc Leu	tac Tyr	gct Ala	gat Asp	atg Met	ggc Gly	835

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His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp Phe Cys Val Val Met				
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cct gct tta atc ttg acg tat ttg ggg cag ggc gcc ttg gtg atc aac	931			
Pro Ala Leu Ile Leu Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn				
265	270	275		
cag cct gaa gcg gtg cgc aac ccc atg ttt tat ctc gcg ccg gaa ggt	979			
Gln Pro Glu Ala Val Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly				
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Leu Arg Ile Pro Leu Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala				
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Asn Leu Lys Leu Leu Pro Arg Met Val Ile Arg His Thr Ser Arg Lys				
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gag gaa ggc cag atc tat atg cca ctg gtt aat gga ttg ctg ttt gta	1171			
Glu Glu Gly Gln Ile Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val				
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Ser Val Met Val Val Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala				
360	365	370		
agc gcg tac gga ctt gca gtg acc gga acc ttg gtg ctg gtc agc gtc	1267			
Ser Ala Tyr Gly Leu Ala Val Thr Gly Thr Leu Val Leu Val Ser Val				
375	380	385		
ctg tat ctg atc tat gtt cac acc aca tgg tgg aaa aca gcg ctg ttc	1315			
Leu Tyr Leu Ile Tyr Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe				
390	395	400	405	
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Ile Val Leu Ile Gly Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr				
410	415	420		
acg aaa att cac gac ggt ggc tgg ctt cca cta ctt att gcg gcc gtg	1411			
Thr Lys Ile His Asp Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val				
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ctc atc gtg gtg atg cgg acc tgg gag tgg gga agt gac cgc gtc aat	1459			
Leu Ile Val Val Met Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn				
440	445	450		
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Gln Glu Arg Ala Glu Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys				
455	460	465		
ctc gat cag cca cac aat att ggt ctg cgt aaa gtt gcc gaa gtg gca	1555			
Leu Asp Gln Pro His Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala				
470	475	480	485	

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Val Phe Pro His Gly Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg
490 495 500

tgc gtg aaa gac ctc aag ctt tta tac cga gag atc gtg atc gtt cga 1651
Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg
505 510 515

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Ile Val Gln Glu His Val Pro His Val Pro Pro Glu Glu Arg Ala Glu
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Met Glu Val Leu His His Ala Pro Ile Arg Val Val Arg Val Asp Leu
535 540 545

cac ctt ggt tat ttt gat gag cag aac ctg cct gag cat ctc cat gcc 1795
His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro Glu His Leu His Ala
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Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr
570 575 580

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Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu
585 590 595

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Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys
600 605 610

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<211> 628

<212> PRT

<213> Corynebacterium glutamicum

<400> 402

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Gln His Asn Lys Val Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile
50 55 60

Ser Met Val Leu Trp Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val
65 70 75 80

Met Leu Val Thr Arg Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala
 85 90 95
 Leu Val Ala Leu Leu Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala
 100 105 110
 Val Ala Gly Met Leu Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile
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 Thr Pro Ala Ile Ser Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile
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 Ser Pro Ser Phe Glu Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu
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 Ile Ala Ile Phe Ala Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys
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 Ala Phe Gly Pro Ile Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu
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 Gly Ile Pro Gln Ile Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser
 195 200 205
 Pro His Trp Ala Leu Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe
 210 215 220
 Val Leu Leu Gly Ala Val Val Leu Thr Val Thr Gly Ala Glu Ala Leu
 225 230 235 240
 Tyr Ala Asp Met Gly His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp
 245 250 255
 Phe Cys Val Val Met Pro Ala Leu Ile Leu Thr Tyr Leu Gly Gln Gly
 260 265 270
 Ala Leu Val Ile Asn Gln Pro Glu Ala Val Arg Asn Pro Met Phe Tyr
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 Ala Thr Val Ile Ala Ser Gln Ala Val Ile Ser Gly Ala Tyr Ser Leu
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 Thr Lys Gln Ala Val Asn Leu Lys Leu Leu Pro Arg Met Val Ile Arg
 325 330 335
 His Thr Ser Arg Lys Glu Glu Gly Gln Ile Tyr Met Pro Leu Val Asn
 340 345 350
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 355 360 365
 Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu Ala Val Thr Gly Thr Leu
 370 375 380
 Val Leu Val Ser Val Leu Tyr Leu Ile Tyr Val His Thr Thr Trp Trp
 385 390 395 400
 Lys Thr Ala Leu Phe Ile Val Leu Ile Gly Ile Pro Glu Val Leu Leu

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405 410 415
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 Ser Asp Arg Val Asn Gln Glu Arg Ala Glu Leu Glu Leu Pro Met Asp
 450 455 460
 Lys Phe Leu Glu Lys Leu Asp Gln Pro His Asn Ile Gly Leu Arg Lys
 465 470 475 480
 Val Ala Glu Val Ala Val Phe Pro His Gly Thr Ser Asp Thr Val Pro
 485 490 495
 Leu Ser Leu Val Arg Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu
 500 505 510
 Ile Val Ile Val Arg Ile Val Gln His Val Pro His Val Pro Pro
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 Glu Glu Arg Ala Glu Met Glu Val Leu His His Ala Pro Ile Arg Val
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 Val Arg Val Asp Leu His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro
 545 550 555 560
 Glu His Leu His Ala Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe
 565 570 575
 Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly
 580 585 590
 Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg
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<222> (1)..(1134)

<223> FRXA02348

<400> 403

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tct	ggc	gca	tat	tca	ttg	acc	aag	cag	gcc	gtg	aat	ttg	aaa	ctg	ctg	240
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Pro	Arg	Met	Val	Ile	Arg	His	Thr	Ser	Arg	Lys	Glu	Glu	Gly	Gln	Ile	
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Ile	Pro	Glu	Val	Leu	Leu	Phe	Ala	Ser	Asn	Thr	Thr	Lys	Ile	His	Asp	
				165					170					175		
ggc	ggc	tgg	ctt	cca	cta	ctt	att	gca	gcc	gtg	ctc	atc	gtg	gtg	atg	576
Gly	Gly	Trp	Leu	Pro	Leu	Leu	Ile	Ala	Ala	Val	Leu	Ile	Val	Val	Met	
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Leu	Glu	Leu	Pro	Met	Asp	Lys	Phe	Leu	Glu	Lys	Leu	Asp	Gln	Pro	His	
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Thr	Ser	Asp	Thr	Val	Pro	Leu	Ser	Leu	Val	Arg	Cys	Val	Lys	Asp	Leu	
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Lys	Leu	Leu	Tyr	Arg	Glu	Ile	Val	Ile	Val	Arg	Ile	Val	Gln	Glu	His	

115					120					125					
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Val	His	Thr	Thr	Trp	Trp	Lys	Thr	Ala	Leu	Phe	Ile	Val	Leu	Ile	Gly
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Ile	Pro	Glu	Val	Leu	Leu	Phe	Ala	Ser	Asn	Thr	Thr	Lys	Ile	His	Asp
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Gly	Gly	Trp	Leu	Pro	Leu	Leu	Ile	Ala	Ala	Val	Leu	Ile	Val	Val	Met
			180					185						190	
Arg	Thr	Trp	Glu	Trp	Gly	Ser	Asp	Arg	Val	Asn	Gln	Glu	Arg	Ala	Glu
			195				200					205			
Leu	Glu	Leu	Pro	Met	Asp	Lys	Phe	Leu	Glu	Lys	Leu	Asp	Gln	Pro	His
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Asn	Ile	Gly	Leu	Arg	Lys	Val	Ala	Glu	Val	Ala	Val	Phe	Pro	His	Gly
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Thr	Ser	Asp	Thr	Val	Pro	Leu	Ser	Leu	Val	Arg	Cys	Val	Lys	Asp	Leu
				245					250					255	
Lys	Leu	Leu	Tyr	Arg	Glu	Ile	Val	Ile	Val	Arg	Ile	Val	Gln	Glu	His
			260					265					270		
Val	Pro	His	Val	Pro	Pro	Glu	Glu	Arg	Ala	Glu	Met	Glu	Val	Leu	His
		275					280					285			
His	Ala	Pro	Ile	Arg	Val	Val	Arg	Val	Asp	Leu	His	Leu	Gly	Tyr	Phe
	290					295					300				
Asp	Glu	Gln	Asn	Leu	Pro	Glu	His	Leu	His	Ala	Ile	Asp	Pro	Thr	Trp
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Asp	Asn	Ala	Thr	Tyr	Phe	Leu	Ser	Ala	Leu	Thr	Leu	Arg	Ser	Arg	Leu
				325					330					335	
Pro	Gly	Lys	Ile	Ala	Gly	Trp	Arg	Asp	Arg	Leu	Tyr	Leu	Ser	Met	Glu
			340					345					350		
Arg	Asn	Gln	Ala	Ser	Arg	Thr	Glu	Ser	Phe	Lys	Leu	Gln	Pro	Ser	Lys
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<222> (101)..(778)

<223> FRXA02344

<400> 405

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Met Leu Asn Arg Met
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aaa agt gcg cgg cca aaa tca gtc gct cca aaa tcc gga caa gct tta 163
Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys Ser Gly Gln Ala Leu
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Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly Asp Ile Gly Thr Ser
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ccc ctg tac tca ctt cac act gca ttc agc atg cag cac aac aaa gtc 259
Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met Gln His Asn Lys Val
40 45 50

gaa gtc act cag gaa aat gtg tac ggc atc atc tcc atg gtg ttg tgg 307
Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile Ser Met Val Leu Trp
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acc atc act ttg atc gtc acc gtc aaa tac gtc atg ctg gtc acc cga 355
Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val Met Leu Val Thr Arg
70 75 80 85

gct gac aac caa gga caa ggt ggc atc ctg gcg ctc gtt gct ttg ctg 403
Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala Leu Val Ala Leu Leu
90 95 100

aaa aac cgt ggg cac tgg gga aaa ttc gtg gca gta gcc ggc atg ttg 451
Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala Val Ala Gly Met Leu
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ggc gcc gca ttg ttt tat ggc gat gtg gtg atc acc ccg gcg atc tct 499
Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile Thr Pro Ala Ile Ser
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gtt ctc agc gca aca gaa ggc ttg acg gtt atc tcc cca agc ttt gag 547
Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile Ser Pro Ser Phe Glu
135 140 145

cgc ttc att ctg ccc gta tct ctc gca gtt ctg atc gct att ttt gca 595
Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu Ile Ala Ile Phe Ala
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atc caa ccg ctc ggt aca gaa aaa gtc ggc aaa gcc ttc ggc ccc atc 643
Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys Ala Phe Gly Pro Ile
170 175 180

atg ttg ctg tgg ttt gtc acc ctt gca gga ttg gga att ccg caa atc 691
Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu Gly Ile Pro Gln Ile
185 190 195

atc ggg cac cca gaa atc ttg cag agc ttg tct cca cat tgg gcc ctg 739
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200 205 210

cgc ttg att gtg gct gag cct ttc caa gca ttt gtg ctg 778
Arg Leu Ile Val Glu Pro Phe Gln Ala Phe Val Leu

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acc ttc gct gtt gtc ttc atg tac gac atg gaa gta ggc gtc ggc ctc 720
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 Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
 245 250 255

ggc gtt ccc ggc gga gcc atc atg gca gca acc ggc atg ctg gcc tcc 816
 Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
 260 265 270

atg ctc gga ttc aac acc gaa caa gtc gcc ctc atg atc gcc gct tac 864
 Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
 275 280 285

atc gcg att gac tcc ttc ggc acc gca gca aac gtc acc ggc gac ggc 912
 Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
 290 295 300

gca atc gca gtc atc gtg aac aaa ttc gcc aag ggc cag ctg cac acc 960
 Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
 305 310 315 320

act tcc cca gat gaa atc gaa gaa gac gac cgc gtt gcc ttc gac atc 1008
 Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile
 325 330 335

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 Thr Pro Ser Asp Val Glu His His Lys
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agt 1058

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 <213> Corynebacterium glutamicum

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 35 40 45

Gln Pro Tyr Phe Asn Ile Glu Met Pro Pro Pro Phe Glu Val Met Thr
 50 55 60

Ala Leu Leu Leu Ala Phe Cys Leu Gly Leu Gly Met Ala Val Ile Lys
 65 70 75 80

Ser Asp Thr Leu Phe Lys Val Thr Arg Glu Leu Glu Arg Val Val Met
 85 90 95

Lys Thr Ile Thr Ala Phe Val Ile Pro Leu Leu Pro Leu Phe Ile Phe
 100 105 110

Gly Ile Phe Leu Gly Met Gly Met Asn Gly Gly Leu Leu Glu Ile Met
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 Ser Ala Phe Gly Lys Val Leu Ile Leu Ala Val Val Gly Thr Leu Leu
 130 135 140
 Phe Leu Ala Ile Gln Phe Ile Ile Ala Gly Ala Val Ser Lys Lys Asn
 145 150 155 160
 Pro Trp Lys Leu Phe Lys Asn Met Leu Pro Ala Tyr Phe Thr Ala Leu
 165 170 175
 Gly Thr Ser Ser Ser Ala Ala Thr Ile Pro Val Thr Tyr Gln Gln Thr
 180 185 190
 Leu Lys Asn Asp Val Asp Val Asn Val Ala Gly Phe Val Val Pro Leu
 195 200 205
 Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe
 210 215 220
 Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu
 225 230 235 240
 Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
 245 250 255
 Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
 260 265 270
 Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
 275 280 285
 Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
 290 295 300
 Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
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<222> (1)..(459)

<223> FRXA00960

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tgc gcc acc atc cac cta gct gga tcg atg atg aag atc ggc ctc ttc 96
 Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe
 20 25 30

acc ttc gct gtt gtc ttc atg tac gac atg gaa gta ggc gtc ggc ctc 144
 Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu
 35 40 45

tcc atc gga ttc ctc ctc atg ctg ggc atc acc atg atc gcc gca cca 192
 Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
 50 55 60

ggc gtt ccc ggc gga gcc atc atg gca gca acc ggc atg ctg gcc tcc 240
 Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
 65 70 75 80

atg ctc gga ttc aac acc gaa caa gtc gcc ctc atg atc gcc gct tac 288
 Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
 85 90 95

atc gcg att gac tcc ttc ggc acc gca gca aac gtc acc ggc gac ggc 336
 Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
 100 105 110

gca atc gca gtc atc gtg aac aaa ttc gcc aag ggc cag ctg cac acc 384
 Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
 115 120 125

act tcc cca gat gaa atc gaa gaa gac gac cgc gtt gcc ttc gac atc 432
 Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile
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 Thr Pro Ser Asp Val Glu His His Lys
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agt 482

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 35 40 45

Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
 50 55 60

Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
 65 70 75 80

Thr Pro Ser Asp Val Glu His His Lys
145 150

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Val Trp Phe Ala Ile Thr Ala Phe Phe Ser Val Leu Ala Gly Ile Ala
105 110 115

gta gcg ctg att atg cag cct ggt gtt gga tcc act gtc gac gca tct 499
 Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser Thr Val Asp Ala Ser
 120 125 130

aat gct gct gat cct tct cgc gtg ggc agc tgg ctg ggc ttt atc cag 547
 Asn Ala Ala Asp Pro Ser Arg Val Gly Ser Trp Leu Gly Phe Ile Gln
 135 140 145

tcc gtt att cca tca aac att ctg gga ctt tcc ggt tct tac agt gag 595
 Ser Val Ile Pro Ser Asn Ile Leu Gly Leu Ser Gly Ser Tyr Ser Glu
 150 155 160 165

aac tct ggt gtg aac ctg tcc ttc aac gtg ctg cag atc ctg gtt atc 643
 Asn Ser Gly Val Asn Leu Ser Phe Asn Val Leu Gln Ile Leu Val Ile
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tcc att gcg att ggt gtt gca gct ctg aag gct ggc aag tcc gcc gag 691
 Ser Ile Ala Ile Gly Val Ala Ala Leu Lys Ala Gly Lys Ser Ala Glu
 185 190 195

cct ttc ttg aag ttc acc gag tcc ttc ctc aag atc atc cag atc gtg 739
 Pro Phe Leu Lys Phe Thr Glu Ser Phe Leu Lys Ile Ile Gln Ile Val
 200 205 210

ttg tgg tgg att att cgc ctg gct cca att ggt tcc gct gcg ctg atc 787
 Leu Trp Trp Ile Ile Arg Leu Ala Pro Ile Gly Ser Ala Ala Leu Ile
 215 220 225

ggt aat gct gtt gct acc tac ggt tgg tct gca ctt gga tcc ctg ggc 835
 Gly Asn Ala Val Ala Thr Tyr Gly Trp Ser Ala Leu Gly Ser Leu Gly
 230 235 240 245

aag ttt gtt ctt gcg atc tac gtt ggt ctg gca atc gtc atg ttc gtt 883
 Lys Phe Val Leu Ala Ile Tyr Val Gly Leu Ala Ile Val Met Phe Val
 250 255 260

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 Ile Tyr Pro Val Val Leu Lys Leu Asn Gly Ile Pro Val Leu Gly Phe
 265 270 275

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 Phe Lys Arg Val Trp Pro Val Thr Ser Leu Gly Phe Val Thr Arg Ser
 280 285 290

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 Ser Met Gly Val Met Pro Val Thr Gln Arg Val Thr Glu Gln Ser Leu
 295 300 305

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 Gly Val Pro Ser Ala Tyr Ala Ser Phe Ala Ile Pro Leu Gly Ala Thr
 310 315 320 325

agc aag atg gac ggc tgc gct gct gtc tac cca gct gtt gcc gct atc 1123
 Ser Lys Met Asp Gly Cys Ala Ala Val Tyr Pro Ala Val Ala Ala Ile
 330 335 340

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 Phe Val Ala Gln Phe Tyr Gly Ile Asp Leu Ser Ile Met Asp Tyr Val
 345 350 355

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Leu Ile Met Ile Val Ser Val Leu Gly Ser Ala Ala Thr Ala Gly Thr
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 act ggc gca acc gtc atg ctg acc ctg acc cta tcc acc ttg ggt ctg 1267
 Thr Gly Ala Thr Val Met Leu Thr Leu Thr Leu Ser Thr Leu Gly Leu
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 390 395 400 405
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 410 415 420
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 Ile Val Ala Lys Arg Glu Gly Ile Leu Asp Gln Asp Val Trp Asp Ala
 425 430 435
 gct gaa aag ggt ggc gct gct att gaa atg gca acc gtc tct gag aaa 1459
 Ala Glu Lys Gly Gly Ala Ala Ile Glu Met Ala Thr Val Ser Glu Lys
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 35 40 45
 Glu Ala Ser Trp Leu Thr Gly Leu Leu Ser Gly Val Gly Ser Ala Tyr
 50 55 60
 Val Ser Leu Leu Lys Val Met Val Pro Pro Leu Val Phe Ala Ala Val
 65 70 75 80
 Val Thr Ser Val Ala Lys Leu Arg Glu Val Ala Asn Ala Ala Arg Leu
 85 90 95
 Ala Val Ser Thr Leu Val Trp Phe Ala Ile Thr Ala Phe Phe Ser Val
 100 105 110
 Leu Ala Gly Ile Ala Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser
 115 120 125
 Thr Val Asp Ala Ser Asn Ala Ala Asp Pro Ser Arg Val Gly Ser Trp

130	135	140
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Gly Ser Tyr Ser Glu Asn Ser Gly Val Asn Leu Ser Phe Asn Val Leu 165 170 175		
Gln Ile Leu Val Ile Ser Ile Ala Ile Gly Val Ala Ala Leu Lys Ala 180 185 190		
Gly Lys Ser Ala Glu Pro Phe Leu Lys Phe Thr Glu Ser Phe Leu Lys 195 200 205		
Ile Ile Gln Ile Val Leu Trp Trp Ile Ile Arg Leu Ala Pro Ile Gly 210 215 220		
Ser Ala Ala Leu Ile Gly Asn Ala Val Ala Thr Tyr Gly Trp Ser Ala 225 230 235 240		
Leu Gly Ser Leu Gly Lys Phe Val Leu Ala Ile Tyr Val Gly Leu Ala 245 250 255		
Ile Val Met Phe Val Ile Tyr Pro Val Val Leu Lys Leu Asn Gly Ile 260 265 270		
Pro Val Leu Gly Phe Phe Lys Arg Val Trp Pro Val Thr Ser Leu Gly 275 280 285		
Phe Val Thr Arg Ser Ser Met Gly Val Met Pro Val Thr Gln Arg Val 290 295 300		
Thr Glu Gln Ser Leu Gly Val Pro Ser Ala Tyr Ala Ser Phe Ala Ile 305 310 315 320		
Pro Leu Gly Ala Thr Ser Lys Met Asp Gly Cys Ala Ala Val Tyr Pro 325 330 335		
Ala Val Ala Ala Ile Phe Val Ala Gln Phe Tyr Gly Ile Asp Leu Ser 340 345 350		
Ile Met Asp Tyr Val Leu Ile Met Ile Val Ser Val Leu Gly Ser Ala 355 360 365		
Ala Thr Ala Gly Thr Thr Gly Ala Thr Val Met Leu Thr Leu Thr Leu 370 375 380		
Ser Thr Leu Gly Leu Pro Leu Ala Gly Val Gly Leu Leu Leu Ala Ile 385 390 395 400		
Glu Pro Ile Ile Asp Met Gly Arg Thr Ala Thr Asn Val Thr Gly Gln 405 410 415		
Ala Leu Val Pro Ala Ile Val Ala Lys Arg Glu Gly Ile Leu Asp Gln 420 425 430		
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gca ttc tcc gag agc atc atc aac cca ttg atc gct tcc atc ggc agc 144
 Ala Phe Ser Glu Ser Ile Ile Asn Pro Leu Ile Ala Ser Ile Gly Ser
 35 40 45

aca gag gtt gaa ggc ctc ggc ttc cac atc cgc gcc ggc aat gcc gca 192
 Thr Glu Val Glu Gly Leu Gly Phe His Ile Arg Ala Gly Asn Ala Ala
 50 55 60

aca ttc gtg gat ttt ggt gct gtc atc acc gca gcg atc aac ttc ctc 240
 Thr Phe Val Asp Phe Gly Ala Val Ile Thr Ala Ala Ile Asn Phe Leu
 65 70 75 80

atc atc gca gca att gtc tac ttc gtt ctc gtt gct cca atg aac aag 288
 Ile Ile Ala Ala Ile Val Tyr Phe Val Leu Val Ala Pro Met Asn Lys
 85 90 95

ctc agc gaa acc ctc gca aag cgc aag ggt gtt gaa gaa gac gag acc 336
 Leu Ser Glu Thr Leu Ala Lys Arg Lys Gly Val Glu Glu Asp Glu Thr
 100 105 110

cca gct tcc atc gaa gca gaa ctc ctc acc gag atc cgc gat ctc ctg 384
 Pro Ala Ser Ile Glu Ala Glu Leu Leu Thr Glu Ile Arg Asp Leu Leu
 115 120 125

cag gag caa aag cgc ctt cag tagttaaag gccctaaaag cac 428
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 35 40 45

Thr Glu Val Glu Gly Leu Gly Phe His Ile Arg Ala Gly Asn Ala Ala
 50 55 60

Thr Phe Val Asp Phe Gly Ala Val Ile Thr Ala Ala Ile Asn Phe Leu
 65 70 75 80

Ile Ile Ala Ala Ile Val Tyr Phe Val Leu Val Ala Pro Met Asn Lys
 85 90 95

Leu Ser Glu Thr Leu Ala Lys Arg Lys Gly Val Glu Glu Asp Glu Thr
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 Met Ile Tyr Arg Arg
 1 5

gtg gga aat tct ggg ctg aag ctt ccg gca att tcg ctt ggg ctg tgg 163
 Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser Leu Gly Leu Trp
 10 15 20

cac aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att 211
 His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile
 25 30 35

cac cgc gcg ttt gat agg gga gtc act cac ttc gat ttg gct aat aac 259
 His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp Leu Ala Asn Asn
 40 45 50

tat gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg 307
 Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu
 55 60 65

cgt gag gat ctc aaa agc cac cgc gat gag ttg atc att tct tcc aag 355
 Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile Ile Ser Ser Lys
 70 75 80 85

gcg ggt tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga 403

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Lys	Tyr	Leu	Val	Ser	Ser	Leu	Asp	Gln	Ser	Leu	Thr	Arg	Leu	Gly	Leu		
			105					110					115				
gat	tac	gtg	gat	att	ttc	tat	cat	cac	cgc	ccg	gat	cca	gat	act	cct	499	
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			120				125					130					
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Leu	Glu	Glu	Thr	Met	Tyr	Ala	Leu	Arg	Asp	Ile	Val	Ala	Ser	Gly	Lys		
			135			140					145						
gct	ctt	tac	gtg	ggc	att	tct	tcc	tac	ggc	cca	gag	ctc	aca	gcg	gag	595	
Ala	Leu	Tyr	Val	Gly	Ile	Ser	Ser	Tyr	Gly	Pro	Glu	Leu	Thr	Ala	Glu		
150					155					160					165		
gcg	gct	gag	ttc	atg	gcg	gag	gag	ggc	tgc	ccg	ctt	ctg	att	cat	cag	643	
Ala	Ala	Glu	Phe	Met	Ala	Glu	Glu	Gly	Cys	Pro	Leu	Leu	Ile	His	Gln		
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cca	agc	tat	tcc	atc	att	aat	cgt	tgg	gtg	gag	gaa	ccg	ggc	gat	gac	691	
Pro	Ser	Tyr	Ser	Ile	Ile	Asn	Arg	Trp	Val	Glu	Glu	Pro	Gly	Asp	Asp		
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ggt	gag	aac	ttg	ttg	cag	tca	gct	gcc	aac	aat	ggt	ctt	ggc	gtc	att	739	
Gly	Glu	Asn	Leu	Leu	Gln	Ser	Ala	Ala	Asn	Asn	Gly	Leu	Gly	Val	Ile		
			200				205					210					
gct	ttc	tca	cca	ctt	gcg	cag	ggc	ctg	ctc	acg	gac	aaa	tat	ctc	gat	787	
Ala	Phe	Ser	Pro	Leu	Ala	Gln	Gly	Leu	Leu	Thr	Asp	Lys	Tyr	Leu	Asp		
			215			220					225						
gga	att	cca	gag	ggc	tcc	cgc	gcc	agc	cag	ggt	aag	tcc	ctg	tct	gag	835	
Gly	Ile	Pro	Glu	Gly	Ser	Arg	Ala	Ser	Gln	Gly	Lys	Ser	Leu	Ser	Glu		
230					235				240						245		
ggc	atg	ttg	aac	gtg	aac	aat	att	gat	atg	gtc	cgc	aag	ctc	aat	gac	883	
Gly	Met	Leu	Asn	Val	Asn	Asn	Ile	Asp	Met	Val	Arg	Lys	Leu	Asn	Asp		
				250				255						260			
atc	gcc	cag	gaa	cgc	ggg	cag	tca	ctt	gcg	cag	atg	gog	ctt	gca	tgg	931	
Ile	Ala	Gln	Glu	Arg	Gly	Gln	Ser	Leu	Ala	Gln	Met	Ala	Leu	Ala	Trp		
			265				270						275				
gtg	ctg	cgc	gag	caa	aga	gag	tac	ggc	gcc	gga	tta	ccg	tgaccagtgc			980	
Val	Leu	Arg	Glu	Gln	Arg	Glu	Tyr	Gly	Ala	Gly	Leu	Pro					
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<210> 416

<211> 290

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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Ser Leu Gly Leu Trp His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr	20	25	30
Gln Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe	35	40	45
Asp Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn	50	55	60
Phe Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu	65	70	75
Ile Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly	85	90	95
Phe Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu	100	105	110
Thr Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro	115	120	125
Asp Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile	130	135	140
Val Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro	145	150	155
Glu Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro	165	170	175
Leu Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu	180	185	190
Glu Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn	195	200	205
Gly Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr	210	215	220
Asp Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly	225	230	235
Lys Ser Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val	245	250	255
Arg Lys Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln	260	265	270
Met Ala Leu Ala Trp Val Leu Arg Glu Gln Arg Glu Tyr Gly Ala Gly	275	280	285
Leu Pro	290		

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<211> 1209

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1186)

<223> FRXA01395

<400> 417

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 Met Ala Val Met Ala
 1 5

tat caa cca gca gac aat cgc tat gac gac atg atc tac cgc agg gtg 163
 Tyr Gln Pro Ala Asp Asn Arg Tyr Asp Asp Met Ile Tyr Arg Arg Val
 10 15 20

gga aat tct ggg ctg aag ctt ccg gca att tcg ctt ggg ctg tgg cac 211
 Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser Leu Gly Leu Trp His
 25 30 35

aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att cac 259
 Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile His
 40 45 50

cgc gcg ttt gat agg gga gtc act cac ttc gat ttg gct aat aac tat 307
 Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp Leu Ala Asn Asn Tyr
 55 60 65

gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg cgt 355
 Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu Arg
 70 75 80 85

gag gat ctc aaa agc cac cgc gat gag ttg atc att tct tcc aag gcg 403
 Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile Ile Ser Ser Lys Ala
 90 95 100

ggg tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga aag 451
 Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe Gly Gly Ser Arg Lys
 105 110 115

tat cta gtg agt tcc ctt gat cag tcc ctg act cgc ctc ggc ttg gat 499
 Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr Arg Leu Gly Leu Asp
 120 125 130

tac gtg gat att ttc tat cat cac cgc ccg gat cca gat act cct ttg 547
 Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp Pro Asp Thr Pro Leu
 135 140 145

gaa gaa acc atg tac gca ttg cgt gac att gtt gcg tct gga aag gct 595
 Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala Ser Gly Lys Ala
 150 155 160 165

ctt tac gtg ggt att tct tcc tac ggt cca gag ctc aca gcg gag gcg 643
 Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu Thr Ala Glu Ala
 170 175 180

gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg att cat cag cca 691
 Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu Ile His Gln Pro
 185 190 195

agc tat tcc atc att aat cgt tgg gtg gag gaa ccg ggc gat gac ggt 739
 Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro Gly Asp Asp Gly
 200 205 210
 gag aac ttg ttg cag tca gct gcc aac aat ggt ctt ggc gtc att gct 787
 Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu Gly Val Ile Ala
 215 220 225
 ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa tat ctc gat gga 835
 Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys Tyr Leu Asp Gly
 230 235 240 245
 att cca gag ggt tcc cgc gcc agc cag ggt aag tcc ctk tst kac ggs 883
 Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser Xaa Xaa Xaa Xaa
 250 255 260
 wtg ttg aac gtg aac aat att gat wtg gtc ccm ars ytn awk rsa wtt 931
 Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa Xaa Xaa Xaa Xaa
 265 270 275
 tcc mar ram acc ggg cag tcc ttt nnc cna aag gnc ttt tgt tgg gtt 979
 Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys Xaa Phe Cys Trp Val
 280 285 290
 gtt gcc caa cca agg aaa gta cgg cgc cgg att acc gtg acc agt gca 1027
 Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile Thr Val Thr Ser Ala
 295 300 305
 ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc ctt gat tca 1075
 Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser Leu Asp Ser
 310 315 320 325
 ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg atc gat gag 1123
 Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala Ile Asp Glu
 330 335 340
 att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc acc gat tcc 1171
 Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala Thr Asp Ser
 345 350 355
 aaa acc cgc gaa aac taacccatca acatcagttt gat 1209
 Lys Thr Arg Glu Asn
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<210> 418

<211> 362

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

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 20 25 30
 Leu Gly Leu Trp His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln
 35 40 45
 Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp

50 55 60
 Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe
 65 70 75 80
 Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile
 85 90 95
 Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe
 100 105 110
 Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr
 115 120 125
 Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp
 130 135 140
 Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val
 145 150 155 160
 Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu
 165 170 175
 Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu
 180 185 190
 Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu
 195 200 205
 Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly
 210 215 220
 Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp
 225 230 235 240
 Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys
 245 250 255
 Ser Xaa Xaa Xaa Xaa Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa
 260 265 270
 Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys
 275 280 285
 Xaa Phe Cys Trp Val Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile
 290 295 300
 Thr Val Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp
 305 310 315 320
 Asn Ser Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu
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 Glu Ala Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala
 340 345 350
 Lys Ala Thr Asp Ser Lys Thr Arg Glu Asn
 355 360

<210> 419

<211> 1911
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1888)
 <223> RXA02597

<400> 419

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                                Leu Pro Glu Gln Asp
                                1                               5

tta acc acc ttg gcc aat gat tgg ctc caa gct ttt gaa aag gcc act 163
Leu Thr Thr Leu Ala Asn Asp Trp Leu Gln Ala Phe Glu Lys Ala Thr
                                10                               15                               20

gct agt tcc agc cct gat gaa gct gcc act gca gtc gtg caa ctt ttt 211
Ala Ser Ser Ser Pro Asp Glu Ala Ala Thr Ala Val Val Gln Leu Phe
                                25                               30                               35

gag gat gaa gga tac tgg cga gac ctt ctt gca ttc acg tgg aac ctc 259
Glu Asp Glu Gly Tyr Trp Arg Asp Leu Leu Ala Phe Thr Trp Asn Leu
                                40                               45                               50

acc acc gct gaa ggt gca gat gaa atc gcc gag atg att cgc aat acg 307
Thr Thr Ala Glu Gly Ala Asp Glu Ile Ala Glu Met Ile Arg Asn Thr
                                55                               60                               65

tgg cca tca agc atc ttc cga aac gtt gag cta aag ggc gaa cca gct 355
Trp Pro Ser Ser Ile Phe Arg Asn Val Glu Leu Lys Gly Glu Pro Ala
                                70                               75                               80                               85

gat gaa gga gat ggt gtc act cgc gta cat ttc tcc tgc gaa tcc gca 403
Asp Glu Gly Asp Gly Val Thr Arg Val His Phe Ser Cys Glu Ser Ala
                                90                               95                               100

gac ttc aag tgc acg ggc att gtc cgc ctt cgt aat ggc aag gcg tgg 451
Asp Phe Lys Cys Thr Gly Ile Val Arg Leu Arg Asn Gly Lys Ala Trp
                                105                               110                               115

acg cta ctc acc tca gct cgt gag ctc ctg gag cac cca gag ccc aag 499
Thr Leu Leu Thr Ser Ala Arg Glu Leu Leu Glu His Pro Glu Pro Lys
                                120                               125                               130

ggg cgc aac cgt gag atg ggc gtc gtc cat gga caa aat gag gac acc 547
Gly Arg Asn Arg Glu Met Gly Val Val His Gly Gln Asn Glu Asp Thr
                                135                               140                               145

cga aat tgg act gac cgc aag aat gat cga caa gca gcg ttg ggt gtc 595
Arg Asn Trp Thr Asp Arg Lys Asn Asp Arg Gln Ala Ala Leu Gly Val
                                150                               155                               160                               165

acc gag cag cca tac acc ctc atc atc ggt ggt gga cag ggt ggc att 643
Thr Glu Gln Pro Tyr Thr Leu Ile Ile Gly Gly Gly Gln Gly Gly Ile
                                170                               175                               180

gcc ttg ggc gca cga ctc aag cga ctt ggt gta ccc gct cta atc att 691

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BGI-131CP

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			185					190					195				
gat	aaa	gca	tct	cgc	ccg	ggc	gac	cag	tgg	cgt	agc	cgt	tac	cat	tct	739	
Asp	Lys	Ala	Ser	Arg	Pro	Gly	Asp	Gln	Trp	Arg	Ser	Arg	Tyr	His	Ser		
		200					205					210					
ctc	tgc	ctg	cac	gat	cca	gtt	tgg	tac	gac	cac	ctg	cct	tac	att	cca	787	
Leu	Cys	Leu	His	Asp	Pro	Val	Trp	Tyr	Asp	His	Leu	Pro	Tyr	Ile	Pro		
		215				220					225						
ttc	cca	gat	cat	tgg	cca	gta	ttt	act	cca	aag	gac	aag	atg	ggt	gac	835	
Phe	Pro	Asp	His	Trp	Pro	Val	Phe	Thr	Pro	Lys	Asp	Lys	Met	Gly	Asp		
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tgg	ctc	gag	cac	tat	gtc	ggc	atc	atg	gat	ttg	gac	tat	tgg	acc	aac	883	
Trp	Leu	Glu	His	Tyr	Val	Gly	Ile	Met	Asp	Leu	Asp	Tyr	Trp	Thr	Asn		
				250				255						260			
acc	gag	tgc	ctg	cgc	gcc	tca	tac	aat	gag	gac	acc	aag	cag	tgg	gat	931	
Thr	Glu	Cys	Leu	Arg	Ala	Ser	Tyr	Asn	Glu	Asp	Thr	Lys	Gln	Trp	Asp		
			265					270					275				
gtg	acg	gtc	aat	cgt	gat	ggc	gcg	gag	tcc	acg	ctc	cac	ccc	acc	caa	979	
Val	Thr	Val	Asn	Arg	Asp	Gly	Ala	Glu	Ser	Thr	Leu	His	Pro	Thr	Gln		
		280					285					290					
cta	gtc	atg	gct	act	gga	atg	tcg	ggc	agc	ccg	aac	aaa	cca	act	ttg	1027	
Leu	Val	Met	Ala	Thr	Gly	Met	Ser	Gly	Ser	Pro	Asn	Lys	Pro	Thr	Leu		
		295				300					305						
cct	ggc	cag	gat	aag	ttc	cag	ggc	gaa	att	cgg	cac	tct	tca	gag	cac	1075	
Pro	Gly	Gln	Asp	Lys	Phe	Gln	Gly	Glu	Ile	Arg	His	Ser	Ser	Glu	His		
310					315					320					325		
ccc	ggc	ggc	gat	gtc	gat	cgc	gat	aag	aac	gtt	gta	gtt	ctg	ggc	gct	1123	
Pro	Gly	Gly	Asp	Val	Asp	Arg	Asp	Lys	Asn	Val	Val	Val	Leu	Gly	Ala		
				330					335					340			
aac	aac	tca	gcc	cac	gac	atc	tgc	gcg	gat	ctt	tat	tcc	aat	ggt	gca	1171	
Asn	Asn	Ser	Ala	His	Asp	Ile	Cys	Ala	Asp	Leu	Tyr	Ser	Asn	Gly	Ala		
			345					350					355				
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Lys	Pro	Val	Met	Ile	Gln	Arg	Ser	Ser	Thr	His	Ile	Val	Arg	Ser	Asp		
		360					365					370					
tcg	ctg	atg	cgc	gaa	gtc	ttc	ggg	cct	ctc	tat	tct	gag	gat	gcc	gtt	1267	
Ser	Leu	Met	Arg	Glu	Val	Phe	Gly	Pro	Leu	Tyr	Ser	Glu	Asp	Ala	Val		
		375				380					385						
gaa	gcc	gga	att	gat	acc	gat	act	gcc	gat	ctc	ctg	ttt	gcg	tcg	tgg	1315	
Glu	Ala	Gly	Ile	Asp	Thr	Asp	Thr	Ala	Asp	Leu	Leu	Phe	Ala	Ser	Trp		
390					395					400					405		
cca	tat	aag	gtg	ctg	cca	ggc	gtg	cag	aag	cag	gct	ttc	gac	aag	atc	1363	
Pro	Tyr	Lys	Val	Leu	Pro	Gly	Val	Gln	Lys	Gln	Ala	Phe	Asp	Lys	Ile		
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cgt	gag	gac	gac	aag	gag	ttc	tac	gac	aag	ctt	gaa	aat	gct	gga	ttc	1411	
Arg	Glu	Asp	Asp	Lys	Glu	Phe	Tyr	Asp	Lys	Leu	Glu	Asn	Ala	Gly	Phe		

425	430	435	
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gct gat gga aag att ccg gtg cgc tcc aat gtc agc att gaa gac gtc Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val Ser Ile Glu Asp Val 470 475 480 485			1555
aag gaa aac tct gtg gtg ctc aca gat ggt act gag ctc cca gct gac Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr Glu Leu Pro Ala Asp 490 495 500			1603
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cag ctg gtt gat cag gaa acc gct gac aag gtc ggc cca tgc tgg ggt Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val Gly Pro Cys Trp Gly 520 525 530			1699
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ttg aag gcg cgc tac gaa ggt atg aac act ccg gtg tac agc aag Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro Val Tyr Ser Lys 585 590 595			1888
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<210> 420

<211> 596

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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			20					25					30		

Val	Val	Gln	Leu	Phe	Glu	Asp	Glu	Gly	Tyr	Trp	Arg	Asp	Leu	Leu	Ala
		35					40					45			

Phe	Thr	Trp	Asn	Leu	Thr	Thr	Ala	Glu	Gly	Ala	Asp	Glu	Ile	Ala	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Met 65	Ile Arg Asn Thr Trp 70	Pro Ser Ser Ile Phe 75
		Arg Asn Val Glu Leu 80
Lys 85	Gly Glu Pro Ala Asp 85	Gly Gly Asp Gly 90
		Val Thr Arg Val His Phe 95
Ser 100	Cys Glu Ser Ala Asp Phe 100	Lys Cys Thr Gly Ile Val Arg 110
		Leu Arg
Asn 115	Gly Lys Ala Trp Thr Leu 120	Thr Ser Ala Arg Glu 125
		Leu Leu Glu
His 130	Pro Glu Pro Lys Gly Arg 135	Asn Arg Glu Met Gly 140
		Val Val His Gly
Gln 145	Asn Glu Asp Thr Arg 150	Asn Trp Thr Asp Arg 155
		Lys Asn Asp Arg Gln 160
Ala 165	Ala Leu Gly Val Thr Glu Gln Pro 170	Tyr Thr Leu Ile Ile Gly 175
		Gly Gly
Gly 180	Gln Gly Gly Ile Ala Leu Gly 185	Ala Arg Leu Lys Arg 190
		Leu Gly Val
Pro 195	Ala Leu Ile Ile Asp Lys 200	Ser Arg Pro Gly Asp 205
		Gln Trp Arg
Ser 210	Arg Tyr His Ser Leu Cys 215	Leu His Asp Pro Val Trp Tyr Asp 220
		His
Leu 225	Pro Tyr Ile Pro Phe 230	Pro Asp His Trp Pro Val Phe Thr Pro 240
		Lys
Asp 245	Lys Met Gly Asp Trp Leu Glu His 250	Tyr Val Gly Ile Met Asp 255
		Leu
Asp 260	Tyr Trp Thr Asn Thr Glu Cys 265	Leu Arg Ala Ser Tyr Asn Glu Asp 270
Thr 275	Lys Gln Trp Asp Val Thr Val 280	Asn Arg Asp Gly Ala Glu Ser Thr 285
Leu 290	His Pro Thr Gln Leu Val Met 295	Ala Thr Gly Met Ser Gly Ser Pro 300
Asn 305	Lys Pro Thr Leu Pro Gly Gln Asp 310	Lys Phe Gln Gly Glu Ile Arg 320
His 325	Ser Ser Glu His Pro Gly Gly Asp 330	Val Asp Arg Asp Lys Asn Val 335
Val 340	Val Leu Gly Ala Asn Asn Ser 345	Ala His Asp Ile Cys Ala Asp Leu 350
Tyr 355	Ser Asn Gly Ala Lys Pro Val 360	Met Ile Gln Arg Ser Ser Thr His 365
Ile 370	Val Arg Ser Asp Ser Leu Met Arg 375	Glu Val Phe Gly Pro Leu Tyr 380

Ser Glu Asp Ala Val Glu Ala Gly Ile Asp Thr Asp Thr Ala Asp Leu
 385 390 395 400
 Leu Phe Ala Ser Trp Pro Tyr Lys Val Leu Pro Gly Val Gln Lys Gln
 405 410 415
 Ala Phe Asp Lys Ile Arg Glu Asp Asp Lys Glu Phe Tyr Asp Lys Leu
 420 425 430
 Glu Asn Ala Gly Phe Leu Leu Asp Phe Gly Asp Asp Asp Ser Gly Leu
 435 440 445
 Phe Leu Lys Tyr Leu Arg Arg Gly Ser Gly Tyr Tyr Ile Asp Val Gly
 450 455 460
 Ala Ser Glu Leu Val Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val
 465 470 475 480
 Ser Ile Glu Asp Val Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr
 485 490 495
 Glu Leu Pro Ala Asp Val Ile Val Leu Ala Thr Gly Tyr Gly Asn Met
 500 505 510
 Asn Asn Trp Val Ala Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val
 515 520 525
 Gly Pro Cys Trp Gly Leu Gly Ser Glu Thr Thr Lys Asp Pro Gly Pro
 530 535 540
 Trp Glu Gly Glu Leu Arg Asn Met Trp Lys Pro Thr Asn Val Asp Ser
 545 550 555 560
 Leu Trp Phe His Gly Gly Asn Leu His Gln Ser Arg His Tyr Ser Arg
 565 570 575
 Tyr Leu Ser Met Gln Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro
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 Val Tyr Ser Lys
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<210> 421

<211> 367

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(367)

<223> RXA01454

<400> 421

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Met Met Leu Ile Val

1

5

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<400> 422
Met Met Leu Ile Val Ala Phe Leu Ile Ala Leu Val Gly His Tyr Leu
  1                               5          10          15
Met Gly Gly Ile Arg Ala Gly Asn Gln Met Thr Gly Gln Lys Ser Phe
          20                      25          30
Val Ser Arg Gly Ala Arg Thr Gln Leu Ala Val Thr Ala Gly Leu Trp
          35                      40          45
Met Leu Val Lys Val Ala Gly Tyr Trp Leu Asp Arg Tyr Asp Leu Leu
          50                      55          60
Thr Lys Glu Asn Ser Thr Phe Thr Gly Ala Ser Tyr Thr Asp Ile Asn
          65                      70          75          80
Ala Gln Leu Pro Ala Lys Ile Ile Leu
          85

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<400> 423

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35 40 45

Val Ile Phe Ala Leu Ile Ala Gly Phe Val Thr Trp Leu Ala Gly Tyr
 50 55 60

Phe Val Thr Lys Leu Arg Pro Asp Glu Met Ser Ala Phe Asp Thr Gln
 65 70 75 80

Ser Pro Val Tyr Gln Tyr Arg Gln Met Ile Glu Asn Ser Leu Arg Arg
 85 90 95

Val Met Val Ile Ile Pro Ile Phe Val Ala Leu Leu Ala Gly Leu Ile
 100 105 110

Gly Gln Arg Ser Trp Arg Thr Val Gln Met Trp Leu Asn Gly Gln Asp
 115 120 125

Phe Gly Val Ser Asp Gln Gln Phe Gly Leu Asp Tyr Gly Phe Tyr Ala
 130 135 140

Phe Asp Leu Pro Met Leu Arg Leu Ile Ala
 145 150

<210> 425

<211> 987

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> RXA02684

<400> 425

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atcttttaag ccccgctggct gcctgggcac gatcgcgggc gtg ctt gct gtg ggc 115
 Val Leu Ala Val Gly
 1 5

ttg gtg ctt gtg ttt gtg gtg acg ctg tgg gcg gat tcg aag ctg aat 163
 Leu Val Leu Val Phe Val Val Thr Leu Trp Ala Asp Ser Lys Leu Asn
 10 15 20

cgc gtg gat gcc acg cct gcg acg cag gtg gcg aac act gcc gga acg 211
 Arg Val Asp Ala Thr Pro Ala Thr Gln Val Ala Asn Thr Ala Gly Thr
 25 30 35

aac tgg ctg ctg gta ggt tcg gat tcg cgg cag ggt tta agt gat gag 259
 Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln Gly Leu Ser Asp Glu
 40 45 50

gat att gag cgg cta ggt acc ggc ggc gat atc ggt gtg ggc cgt acg 307
 Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile Gly Val Gly Arg Thr
 55 60 65

gac acg atc atg gtg ttg cat atg ccg cgt act ggc gag ccg acg ctg 355
 Asp Thr Ile Met Val Leu His Met Pro Arg Thr Gly Glu Pro Thr Leu
 70 75 80 85

ttg tcg att ccg cgt gat tct tat gtc aat gtc cct ggc tgg ggc atg 403

Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val Pro Gly Trp Gly Met
 90 95 100
 gat aag gca aac gcc gca ttt acc gtg ggt ggc ccg gaa ctg ctg acg 451
 Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly Pro Glu Leu Leu Thr
 105 110 115
 caa acc gtg gag gag gca act ggc ctg cga att gat cac tat gca gaa 499
 Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile Asp His Tyr Ala Glu
 120 125 130
 atc ggc atg ggt ggt ttg gcg aac atg gtt gat gcc gtg ggc ggc gtg 547
 Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp Ala Val Gly Gly Val
 135 140 145
 gaa atg tgt cct gct gag ccg atg tat gat ccg ctc gcg aac ctg gat 595
 Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro Leu Ala Asn Leu Asp
 150 155 160 165
 att cag gct ggt tgc cag gaa ttt gat ggg gca gcc gcg ctg ggt tat 643
 Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala Ala Ala Leu Gly Tyr
 170 175 180
 gtg cgc act cgt gcc aca gcc ctg ggt gat ctg gac cgg gtg gtg cgt 691
 Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu Asp Arg Val Val Arg
 185 190 195
 cag cgg gaa ttc ttc tcc gct ctg ctg agt aca gct acg tcc ccg ggc 739
 Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr Ala Thr Ser Pro Gly
 200 205 210
 acg ttg ctg aat ccg ttc cgc acc ttc ccg atg atc tcc aac gcg gtg 787
 Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met Ile Ser Asn Ala Val
 215 220 225
 gga aca ttc acc gtc ggc gag ggc gat cac gtg tgg cac ctg gcc cga 835
 Gly Thr Phe Thr Val Gly Glu Gly Asp His Val Trp His Leu Ala Arg
 230 235 240 245
 ttg gcg ctg gcg atg cgc gga gga atc gtg acg gag acc gtg ccg att 883
 Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr Glu Thr Val Pro Ile
 250 255 260
 gcc tca ttc gca gat tac gat gtg gga aat gtt gcg att tgg gac gaa 931
 Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val Ala Ile Trp Asp Glu
 265 270 275
 gct gga gcc gaa gca cta ttt agc tcc atg cgc taaaacocca ggtaatcggt 984
 Ala Gly Ala Glu Ala Leu Phe Ser Ser Met Arg
 280 285
 cac 987

<210> 426

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Val Leu Ala Val Gly Leu Val Leu Val Phe Val Val Thr Leu Trp Ala

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Asn Thr Ala Gly Thr Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln	35	40	45
Gly Leu Ser Asp Glu Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile	50	55	60
Gly Val Gly Arg Thr Asp Thr Ile Met Val Leu His Met Pro Arg Thr	65	70	75
Gly Glu Pro Thr Leu Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val	85	90	95
Pro Gly Trp Gly Met Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly	100	105	110
Pro Glu Leu Leu Thr Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile	115	120	125
Asp His Tyr Ala Glu Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp	130	135	140
Ala Val Gly Gly Val Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro	145	150	155
Leu Ala Asn Leu Asp Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala	165	170	175
Ala Ala Leu Gly Tyr Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu	180	185	190
Asp Arg Val Val Arg Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr	195	200	205
Ala Thr Ser Pro Gly Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met	210	215	220
Ile Ser Asn Ala Val Gly Thr Phe Thr Val Gly Glu Gly Asp His Val	225	230	235
Trp His Leu Ala Arg Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr	245	250	255
Glu Thr Val Pro Ile Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val	260	265	270
Ala Ile Trp Asp Glu Ala Gly Ala Glu Ala Leu Phe Ser Ser Met Arg	275	280	285

<210> 427

<211> 522

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(499)

<223> RXN02391

<400> 427

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                                         Met Thr Gln Ser Asp
                                         1 5

tta ccc gat gat gtt cag gaa ttg gtc act aag atc ttt gga ctg gca 163
Leu Pro Asp Asp Val Gln Glu Leu Val Thr Lys Ile Phe Gly Leu Ala
                        10 15 20

cgt gat ggg gga gca gaa tcc gca gca acc ctc ggt gca tat gtc gac 211
Arg Asp Gly Gly Ala Glu Ser Ala Ala Thr Leu Gly Ala Tyr Val Asp
                        25 30 35

aac ggc gtt gac gtt aac ctg tcc aac caa gat ggc aac act ttg ctc 259
Asn Gly Val Asp Val Asn Leu Ser Asn Gln Asp Gly Asn Thr Leu Leu
                        40 45 50

atg ctc gca gca tat gca gga cat gct gat gtc gtg cag gcg ttg att 307
Met Leu Ala Ala Tyr Ala Gly His Ala Asp Val Val Gln Ala Leu Ile
                        55 60 65

gag cgt ggc gcc gat gtg gat cgc gtg aac aac cgc aat cag acg ccg 355
Glu Arg Gly Ala Asp Val Asp Arg Val Asn Asn Arg Asn Gln Thr Pro
                        70 75 80 85

ctg gcg ggc gcg atc ttt aag aag gaa gaa gcc gtc att gag gca ctg 403
Leu Ala Gly Ala Ile Phe Lys Lys Glu Glu Ala Val Ile Glu Ala Leu
                        90 95 100

ctt gct ggt ggt gct gac cca tac gct gga act cca act gct gtt gat 451
Leu Ala Gly Gly Ala Asp Pro Tyr Ala Gly Thr Pro Thr Ala Val Asp
                        105 110 115

acc gcc aag atg ttt ggc cgc gag gat ctc gta gct cgc ttc gag tca 499
Thr Ala Lys Met Phe Gly Arg Glu Asp Leu Val Ala Arg Phe Glu Ser
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taggccggtg gactggaccg ctt 522

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<210> 428

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

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Gly Ala Tyr Val Asp Asn Gly Val Asp Val Asn Leu Ser Asn Gln Asp

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<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(2803)
<223> RXN02549
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				Met	Val	His	Ala	Lys	5							
				1												
cag	act	aag	aag	cca	ctt	ccc	cgt	ttt	ctt	cac	tcg	gcg	cat	ttc	tat	163
Gln	Thr	Lys	Lys	Pro	Leu	Pro	Arg	Phe	Leu	His	Ser	Ala	His	Phe	Tyr	
				10				15						20		
gtc	tgg	att	gtg	ctg	ggt	ttt	gtg	gtg	ttt	gcg	caa	cct	tat	ggt	cag	211
Val	Trp	Ile	Val	Leu	Gly	Phe	Val	Val	Phe	Ala	Gln	Pro	Tyr	Gly	Gln	
			25					30					35			
gtt	gct	gcc	gat	act	aaa	cta	gat	ttg	ctg	ctc	aac	ccc	gca	gga	ttt	259
Val	Ala	Ala	Asp	Thr	Lys	Leu	Asp	Leu	Leu	Leu	Asn	Pro	Ala	Gly	Phe	
		40					45					50				
tta	acc	ggt	gcg	ctt	cat	gcg	tgg	act	gac	acg	ttc	acc	ttg	ggt	cag	307
Leu	Thr	Gly	Ala	Leu	His	Ala	Trp	Thr	Asp	Thr	Phe	Thr	Leu	Gly	Gln	
	55					60					65					
ttg	caa	aac	caa	gct	tat	ggc	tat	ctg	ttt	ccc	caa	ggg	ttt	ttc	ttc	355
Leu	Gln	Asn	Gln	Ala	Tyr	Gly	Tyr	Leu	Phe	Pro	Gln	Gly	Phe	Phe	Phe	
	70				75					80					85	
ctc	ata	act	gat	ttc	ctc	cct	gac	tgg	att	gcg	cag	cga	ctg	tgg	tgg	403
Leu	Ile	Thr	Asp	Phe	Leu	Pro	Asp	Trp	Ile	Ala	Gln	Arg	Leu	Trp	Trp	
				90					95					100		

tgg ctt gtt ctt ggc ctg gga ttt tct gga ttc tac gca ctg gta gcc 451
 Trp Leu Val Leu Gly Leu Gly Phe Ser Gly Phe Tyr Ala Leu Val Ala
 105 110 115

cgg ctg ggg att ggc aat cct gca ttc agg gtg atc gcc gcg ctg ctg 499
 Arg Leu Gly Ile Gly Asn Pro Ala Phe Arg Val Ile Ala Ala Leu Leu
 120 125 130

ttt gct ctg tcc ccg cgc acg ctc acc acc ctc act gca atc tcc tcc 547
 Phe Ala Leu Ser Pro Arg Thr Leu Thr Thr Leu Thr Ala Ile Ser Ser
 135 140 145

gaa act tgg cct atc atg ctc gcg cca tgg gta tgt ctg cct ctg ctt 595
 Glu Thr Trp Pro Ile Met Leu Ala Pro Trp Val Cys Leu Pro Leu Leu
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tcg cga aat gtg gat gca cgg gcc atc gcg ttg tcc tta ctt ccc gcg 643
 Ser Arg Asn Val Asp Ala Arg Ala Ile Ala Leu Ser Leu Leu Pro Ala
 170 175 180

gca tgc atg ggt gca gtt aat gcc acc gcc acg atg gca gca ctc atc 691
 Ala Cys Met Gly Ala Val Asn Ala Thr Ala Thr Met Ala Ala Leu Ile
 185 190 195

ccg gca gcg ctg atc ttg ctg tat aga ggg ctc ttc tta agg ctg ctt 739
 Pro Ala Ala Leu Ile Leu Leu Tyr Arg Gly Leu Phe Leu Arg Leu Leu
 200 205 210

ctg tgg gga atg ggc gtt ctc gct gtt aat tca tgg tgg atc gga cct 787
 Leu Trp Gly Met Gly Val Leu Ala Val Asn Ser Trp Trp Ile Gly Pro
 215 220 225

ttg ttg gtg ctt ggc aaa tac gcc ccg ccc ttc acc gaa ttc atc gaa 835
 Leu Leu Val Leu Gly Lys Tyr Ala Pro Pro Phe Thr Glu Phe Ile Glu
 230 235 240 245

agt tcc tcc gtc acc act tcc tgg ctc aac cca gta gaa ata ctc cgc 883
 Ser Ser Ser Val Thr Thr Ser Trp Leu Asn Pro Val Glu Ile Leu Arg
 250 255 260

gga acc acc agt tgg aca ccc ttc gta gac act gaa cga caa gcc gga 931
 Gly Thr Thr Ser Trp Thr Pro Phe Val Asp Thr Glu Arg Gln Ala Gly
 265 270 275

tat ctc ctg gtc aac gat gct ctc ttt gtc acc ctc agc gtt ctc gtc 979
 Tyr Leu Leu Val Asn Asp Ala Leu Phe Val Thr Leu Ser Val Leu Val
 280 285 290

gca gcc ctc ggc ttg atc ggc ctc acc ttg atg aaa cac cgt gga ctg 1027
 Ala Ala Leu Gly Leu Ile Gly Leu Thr Leu Met Lys His Arg Gly Leu
 295 300 305

tgg gca ttc atg ctg gcc atc gga ctc ctc atc ctc ggc agc gcc cac 1075
 Trp Ala Phe Met Leu Ala Ile Gly Leu Leu Ile Leu Gly Ser Ala His
 310 315 320 325

cta acg gct gtt caa gaa ttc ctc gac ggc cca ggc gca gca ctt cga 1123
 Leu Thr Ala Val Gln Glu Phe Leu Asp Gly Pro Gly Ala Ala Leu Arg
 330 335 340

aac atc cac aaa ttt gat cta tta gtc cgc atg ccg ttg atg gtg ggc 1171
 Asn Ile His Lys Phe Asp Leu Leu Val Arg Met Pro Leu Met Val Gly
 345 350 355

gtt gcc gca ttg ggg tcg cat atc agt ctg ccc ttg ctt ggg acg act 1219
 Val Ala Ala Leu Gly Ser His Ile Ser Leu Pro Leu Leu Gly Thr Thr
 360 365 370

gca ttg acc agc gga caa ggc aaa cac cac acc atc ccg ctg cct ctc 1267
 Ala Leu Thr Ser Gly Gln Gly Lys His His Thr Ile Pro Leu Pro Leu
 375 380 385

caa aaa cgc caa gcc gca gga ctc ctc gtg gtg atc atc gct gtc ggt 1315
 Gln Lys Arg Gln Ala Ala Gly Leu Leu Val Val Ile Ile Ala Val Gly
 390 395 400 405

gct ctt gct ccc gca tgg tcg gca cgg ctg cta cct cag gga acg tgg 1363
 Ala Leu Ala Pro Ala Trp Ser Ala Arg Leu Leu Pro Gln Gly Thr Trp
 410 415 420

gat gaa gtg cct gac tac tgg tac gaa gcc aca gaa ttc ctc aac caa 1411
 Asp Glu Val Pro Asp Tyr Trp Tyr Glu Ala Thr Glu Phe Leu Asn Gln
 425 430 435

aac gcc aca ggc acc cgc acg ttg att tgg cct agc tcg ccg ttt gcc 1459
 Asn Ala Thr Gly Thr Arg Thr Leu Ile Trp Pro Ser Ser Pro Phe Ala
 440 445 450

cgc cag gac tgg gga tgg act cgg gat gaa cca gct caa cca ctt ctt 1507
 Arg Gln Asp Trp Gly Trp Thr Arg Asp Glu Pro Ala Gln Pro Leu Leu
 455 460 465

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 Asp Val Pro Trp Ala Val Arg Asp Ala Ile Pro Leu Val Pro Pro Glu
 470 475 480 485

gcg att cgc gga tta gat ggt ctc gac gac cta ggc act cta ggc acc 1603
 Ala Ile Arg Gly Leu Asp Gly Leu Asp Asp Leu Gly Thr Leu Gly Thr
 490 495 500

ggt cta aac gac gag gct tta aaa cgt cta ggc atc ggc gca gta ctg 1651
 Gly Leu Asn Asp Glu Ala Leu Lys Arg Leu Gly Ile Gly Ala Val Leu
 505 510 515

gtg agg cat gat ctg gaa gcc gac cca gat att gag gtg gat ctg cct 1699
 Val Arg His Asp Leu Glu Ala Asp Pro Asp Ile Glu Val Asp Leu Pro
 520 525 530

ggg gaa aag cac act ttt ggc tcc caa ggc caa gta gac gtc tac ctc 1747
 Gly Glu Lys His Thr Phe Gly Ser Gln Gly Gln Val Asp Val Tyr Leu
 535 540 545

acc gac ccc gac cgc aat atg tgg atc act tcc ggc aca tcc aag cag 1795
 Thr Asp Pro Asp Arg Asn Met Trp Ile Thr Ser Gly Thr Ser Lys Gln
 550 555 560 565

ctg ccc acc gtc gct ggc ggc ggc gaa atc ctc tcg ctc cta gac acc 1843
 Leu Pro Thr Val Ala Gly Gly Gly Glu Ile Leu Ser Leu Leu Asp Thr
 570 575 580

atc aac ggc tat tcc ccg agg act ttg gtg agt gag aat gcc cag atc 1891

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			585					590					595			
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Val	Thr	Asp	Thr	Pro	Gln	Leu	Val	Gly	Thr	Asn	Tyr	Gly	Asp	Gly	Thr	
		600					605					610				
agt	tcc	gca	gca	ttg	gcc	agc	ctt	gat	gag	act	gag	gtg	aaa	aac	cgc	1987
Ser	Ser	Ala	Ala	Leu	Ala	Ser	Leu	Asp	Glu	Thr	Glu	Val	Lys	Asn	Arg	
	615					620					625					
atc	gtg	gat	tat	cct	tcc	gcg	ggg	cca	atg	acg	cag	gtg	gtg	cag	gaa	2035
Ile	Val	Asp	Tyr	Pro	Ser	Ala	Gly	Pro	Met	Thr	Gln	Val	Val	Gln	Glu	
	630				635					640					645	
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Gly	Ser	Ile	Thr	Ala	Ser	Ser	Ser	Gly	Ser	Asp	Ala	Thr	Ser	Phe	Gly	
			650					655						660		
ggc	gcg	gat	cct	gat	cgt	tcc	ctt	aat	tca	ctt	ctt	gat	cat	cgt	tac	2131
Gly	Ala	Asp	Pro	Asp	Arg	Ser	Leu	Asn	Ser	Leu	Leu	Asp	His	Arg	Tyr	
			665					670					675			
aac	acc	gcc	tgg	tac	ccg	aca	cct	ggc	gat	acg	tct	ccg	tgg	ctc	gaa	2179
Asn	Thr	Ala	Trp	Tyr	Pro	Thr	Pro	Gly	Asp	Thr	Ser	Pro	Trp	Leu	Glu	
		680					685					690				
gtc	tcc	ggg	acc	ggc	acc	aca	tta	tcg	atc	tcc	ccc	cgc	agc	acc	gtc	2227
Val	Ser	Gly	Thr	Gly	Thr	Thr	Leu	Ser	Ile	Ser	Pro	Arg	Ser	Thr	Val	
		695				700					705					
acc	gcc	acc	atc	acc	tcc	ggc	gat	tcc	gtg	atg	gtc	cgc	gag	ttc	gaa	2275
Thr	Ala	Thr	Ile	Thr	Ser	Gly	Asp	Ser	Val	Met	Val	Arg	Glu	Phe	Glu	
	710				715				720						725	
aaa	ggc	cgc	acc	acc	aca	gtt	acg	ttg	gcg	gag	cct	gaa	gct	cgc	att	2323
Lys	Gly	Arg	Thr	Thr	Thr	Val	Thr	Leu	Ala	Glu	Pro	Glu	Ala	Arg	Ile	
			730				735							740		
gaa	ttc	gat	ggg	ttc	gta	gga	att	tcc	gag	ctg	tcc	cta	gag	ggg	ctc	2371
Glu	Phe	Asp	Gly	Phe	Val	Gly	Ile	Ser	Glu	Leu	Ser	Leu	Glu	Gly	Leu	
			745				750						755			
agc	cgc	acc	atc	act	gtg	ccg	gag	acc	tct	cct	gac	gtg	cag	caa	ttc	2419
Ser	Arg	Thr	Ile	Thr	Val	Pro	Glu	Thr	Ser	Pro	Asp	Val	Gln	Gln	Phe	
		760				765					770					
gtt	ttc	caa	cgc	ctc	aca	gtg	ccc	acc	tcg	ttc	ctc	gac	cgc	act	ttc	2467
Val	Phe	Gln	Arg	Leu	Thr	Val	Pro	Thr	Ser	Phe	Leu	Asp	Arg	Thr	Phe	
		775				780					785					
aca	gtc	ccc	cgc	cac	atg	tcc	gtc	acc	gtg	gag	gcc	caa	tcc	tgc	gtc	2515
Thr	Val	Pro	Arg	His	Met	Ser	Val	Thr	Val	Glu	Ala	Gln	Ser	Cys	Val	
	790				795				800						805	
aca	ttg	gaa	ctc	gac	ggc	gat	cgc	atc	gac	tgt	ggc	ccc	tcg	aac	tca	2563
Thr	Leu	Glu	Leu	Asp	Gly	Asp	Arg	Ile	Asp	Cys	Gly	Pro	Ser	Asn	Ser	
			810				815							820		
ccc	ccg	gaa	ccc	aca	cgc	tgc	gca	ccc	aat	cgg	aat	ggg	tca	ccc	tca	2611
Pro	Pro	Glu	Pro	Thr	Arg	Cys	Ala	Pro	Asn	Arg	Asn	Gly	Ser	Pro	Ser	

825	830	835	
cgc aat ccg ctc cgc tcg ccg ctg ttc agc cag caa caa aca tcg agg			2659
Pro Asn Pro Leu Arg Ser Pro Leu Phe Ser Gln Gln Gln Thr Ser Arg			
840	845	850	
cag cac cca ccg acc gcg tgc tcg tca cca cgc gcg ctt tca att cag			2707
Gln His Pro Pro Thr Ala Cys Ser Ser Pro Arg Ala Leu Ser Ile Gln			
855	860	865	
gta cca gcg cgc tta tcg acg cca ccc ccc ttt ccc caa tcc aac tcg			2755
Val Pro Ala Arg Leu Ser Thr Pro Pro Pro Phe Pro Gln Ser Asn Ser			
870	875	880	885
acg cct cct ccc aag gtt tca tca tcc ccg cga acg cct ccg gcg agt			2803
Thr Pro Pro Pro Lys Val Ser Ser Ser Pro Arg Thr Pro Pro Ala Ser			
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<210> 430

<211> 901

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

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			20					25					30		

Gln	Pro	Tyr	Gly	Gln	Val	Ala	Ala	Asp	Thr	Lys	Leu	Asp	Leu	Leu	Leu
		35					40					45			

Asn	Pro	Ala	Gly	Phe	Leu	Thr	Gly	Ala	Leu	His	Ala	Trp	Thr	Asp	Thr
50						55					60				

Phe	Thr	Leu	Gly	Gln	Leu	Gln	Asn	Gln	Ala	Tyr	Gly	Tyr	Leu	Phe	Pro
65					70				75						80

Gln	Gly	Phe	Phe	Phe	Leu	Ile	Thr	Asp	Phe	Leu	Pro	Asp	Trp	Ile	Ala
			85						90					95	

Gln	Arg	Leu	Trp	Trp	Trp	Leu	Val	Leu	Gly	Leu	Gly	Phe	Ser	Gly	Phe
		100						105					110		

Tyr	Ala	Leu	Val	Ala	Arg	Leu	Gly	Ile	Gly	Asn	Pro	Ala	Phe	Arg	Val
	115						120					125			

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Thr	Ala	Ile	Ser	Ser	Glu	Thr	Trp	Pro	Ile	Met	Leu	Ala	Pro	Trp	Val
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Cys	Leu	Pro	Leu	Leu	Ser	Arg	Asn	Val	Asp	Ala	Arg	Ala	Ile	Ala	Leu
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Ser	Leu	Leu	Pro	Ala	Ala	Cys	Met	Gly	Ala	Val	Asn	Ala	Thr	Ala	Thr
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 Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln Gly Gln
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 545 550 555 560
 Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu Ile Leu
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 Ser Leu Leu Asp Thr Ile Asn Gly Tyr Ser Pro Arg Thr Leu Val Ser
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 Tyr Gly Asp Gly Thr Ser Ser Ala Ala Leu Ala Ser Leu Asp Glu Thr
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 Pro Glu Ala Arg Ile Glu Phe Asp Gly Phe Val Gly Ile Ser Glu Leu
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 Leu Asp Arg Thr Phe Thr Val Pro Arg His Met Ser Val Thr Val Glu
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002290-420050

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Thr	Phe	Leu	Met	Phe	Arg	Pro	Val	Leu	Asp	Trp	Gln	Arg	Ser	Pro	Glu	
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Asp	His	Asp	Arg	Asn	Met	Val	Arg	Asn	Leu	Val	Met	Arg	Ile	Pro	Ile	
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Tyr	Gln	Ala	Ile	Leu	Cys	Ala	Val	Val	Trp	Leu	Ile	Gly	Ile	Ala	Ile	
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 Gly Tyr Leu Gly Asn Arg Leu Val Val Ser Ser Val Val Asp Pro Ile
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 Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala Leu
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 Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val Glu
 330 335 340

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 Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp Ala
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Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr Gly
 360 365 370

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 His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp Leu
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 Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala Gly
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 His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp Ala
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 Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro Gly
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cgc acc gtc acc aac gct tcc acg ctg cgt gag gcc aac gag gcg gag 1459
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Ser Tyr Leu Pro Ala Val Gly Phe Ala Tyr Leu Ala Phe Ala Ile Val
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Gln Arg Ser Pro Glu Asp His Asp Arg Asn Met Val Arg Asn Leu Val
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His	Val	Val	Ala	Gly	His	Ile	Gly	Gly	His	Ala	Arg	Phe	Glu	Tyr	Thr	
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Val	Ile	Gly	Asp	Ala	Val	Asn	Gln	Ala	Ala	Arg	Leu	Thr	Glu	Ile	Ala	
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Val Leu Ser Pro Asp 1 5																
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Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe Leu Thr Phe Thr Val 10 15 20																
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Arg Met Val Leu Val Lys Pro Met Val Asn Thr Met Arg Ser Gln Arg 25 30 35																
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Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala Ile Arg Glu Lys Tyr 40 45 50																
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Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr Arg Lys Leu Gln Lys 55 60 65																
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Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu Pro Met Leu Val Gln 70 75 80 85																
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Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu Val Gln Ser Phe Leu																

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Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys Arg Ala Ala Lys Arg			
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 100 105 110
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 Tyr Ile Thr Met Pro Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp
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 Ile Val Val Ala Thr His Met Asn Ala Arg Leu Ser Val Asn Arg Gln
 180 185 190
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 Pro Ala Thr Ile Leu Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu
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<223> RXS01658

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cca Pro 225	act Thr	gtg Val	att Ile	gat Asp	ggg Gly 230	cgc Arg	atc Ile	aag Lys	tgg Trp	atc Ile 235	gtc Val	gat Asp	ggc Gly	tac Tyr	acc Thr 240	720
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Ser	Ser	Asp	Pro 420	Val	Thr	Tyr	Gly	Glu 425	Ile	Thr	Val	Arg	Val 430	Leu	Pro	
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Thr	Asp	Ser 435	Val	Thr	Gln	Gly 440	Pro	Lys	Gln	Ala	Gln	Asp 445	Ala	Met	Met	
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Ser	Ser 450	Asp	Gln	Val	Ala 455	Gln	Asp	Gln	Thr	Leu	Trp 460	Arg	Gly	Ser	Asn	
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Asp 465	Leu	His	Asn	Gly 470	Asn	Leu	Leu	Thr	Leu	Pro 475	Val	Gly	Gly	Gly	Glu 480	
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Ile	Leu	Tyr	Val	Glu	Pro	Ile	Tyr	Ser	Gln	Arg	Lys	Asp	Gln	Ala	Ser	

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 Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
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Glu	Ile	Ser	Asp	Glu	Leu	Arg	Ala	His	Leu	Arg	Tyr	Pro	Glu	Asp	Leu
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Phe	Lys	Val	Gln	Arg	Asp	Met	Leu	Ala	Lys	Tyr	Asn	Val	Asp	Asp	Ser
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Pro	Phe	Arg	Gly	Leu	Gln	Arg	Glu	Tyr	Leu	Ser	Ala	His	Met	Ser	Ala
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Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile Ile Ala Val Leu Leu
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Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn Ala Ser Asp Thr Ala
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 Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp Ser Asp Leu Thr Ser
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 Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile Lys Leu Ala Gly Asp
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ctt gga cta gac gaa tcg aaa ttc act gcc gat ttc caa tcc cct gaa 691
 Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp Phe Gln Ser Pro Glu
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 Ser Asp Leu Thr Ser Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala
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 Val Gly Asp Val Asp Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr
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 Gln Cys Pro Phe Cys Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met
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 Met Lys His Val Glu Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val
 115 120 125
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 Lys Leu Ala Gly Asp Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp
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 Gly Ile Asp Leu Gly Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly
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Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu																195
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Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val																210
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		40					45					50				
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Gly	Leu	Thr	Leu	Thr	Val	Pro	Asp	Phe	Gln	Met	Val	Leu	Lys	Arg	Pro	
	55					60					65					
ctg	cct	atc	ttg	atc	ggt	gta	gta	gcg	cag	ttt	gtc	atc	atg	cca	ttc	355
Leu	Pro	Ile	Leu	Ile	Gly	Val	Val	Ala	Gln	Phe	Val	Ile	Met	Pro	Phe	
	70				75				80						85	
ctg	gcg	atc	gtg	gtt	gcg	aaa	atg	ttc	aac	ctc	aac	cca	gca	ctc	gcc	403
Leu	Ala	Ile	Val	Val	Ala	Lys	Met	Phe	Asn	Leu	Asn	Pro	Ala	Leu	Ala	
				90					95					100		
gtt	ggc	ctt	ctc	atg	ctg	gga	tcc	gtt	ccg	ggt	ggc	acc	tcc	tcc	aat	451
Val	Gly	Leu	Leu	Met	Leu	Gly	Ser	Val	Pro	Gly	Gly	Thr	Ser	Ser	Asn	
			105					110					115			
gtg	att	gcg	ttt	ctc	gcc	cga	gga	gat	gtc	gcg	cta	tcg	gtc	acc	atg	499
Val	Ile	Ala	Phe	Leu	Ala	Arg	Gly	Asp	Val	Ala	Leu	Ser	Val	Thr	Met	
		120					125					130				
acc	tct	gtg	tcc	acc	att	gtt	tcc	cca	atc	atg	acg	cct	ttc	ctc	atg	547
Thr	Ser	Val	Ser	Thr	Ile	Val	Ser	Pro	Ile	Met	Thr	Pro	Phe	Leu	Met	
	135					140					145					
ctc	atg	ctg	gca	ggt	act	gaa	acc	gcc	gtc	gat	ggt	gga	ggc	atg	gcg	595
Leu	Met	Leu	Ala	Gly	Thr	Glu	Thr	Ala	Val	Asp	Gly	Gly	Gly	Met	Ala	
	150				155					160				165		
tgg	act	ttg	gta	caa	aca	gtg	ctg	ctg	cct	gtg	atc	atc	ggc	cta	gtt	643
Trp	Thr	Leu	Val	Gln	Thr	Val	Leu	Leu	Pro	Val	Ile	Ile	Gly	Leu	Val	
			170					175						180		
ctg	cgt	gtc	ttc	ttg	aac	aag	tgg	atc	gac	aag	att	ttg	ccg	atc	ctt	691
Leu	Arg	Val	Phe	Leu	Asn	Lys	Trp	Ile	Asp	Lys	Ile	Leu	Pro	Ile	Leu	
			185					190					195			
cct	tat	ctc	tcc	atc	ctc	ggt	atc	ggt	ggc	gtg	gtg	ttc	ggc	gca	gtc	739
Pro	Tyr	Leu	Ser	Ile	Leu	Gly	Ile	Gly	Gly	Val	Val	Phe	Gly	Ala	Val	
		200					205					210				
gca	gcc	aac	gcg	gaa	cga	ctc	gtg	tct	gtc	gga	ctc	atc	gtg	ttc	gtt	787
Ala	Ala	Asn	Ala	Glu	Arg	Leu	Val	Ser	Val	Gly	Leu	Ile	Val	Phe	Val	
		215				220					225					
gca	gtt	atc	gtg	cac	aac	gta	ctt	gga	tac	gtt	gtg	gga	tac	ctc	acc	835
Ala	Val	Ile	Val	His	Asn	Val	Leu	Gly	Tyr	Val	Val	Gly	Tyr	Leu	Thr	
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Gly	Arg	Val														

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<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 442

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Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile
 35 40 45

Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met
 50 55 60

Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe
 65 70 75 80

Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu
 85 90 95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly
 100 105 110

Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala
 115 120 125

Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met
 130 135 140

Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp
 145 150 155 160

Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val
 165 170 175

Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys
 180 185 190

Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val
 195 200 205

Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly
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Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val
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Val Gly Tyr Leu Thr Gly Arg Val
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<212> DNA

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<220>

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<222> (101)..(1366)

<223> RXS00654

<400> 443

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tgctgtgaag tgccacctgt ttggaaaggc gaacacgata gtg ctc gat att ttg 115
Val Leu Asp Ile Leu
1 5

att tac ccg gtg tct gga gtg atg aag ctg tgg cac ctg ctt ctt cac 163
Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp His Leu Leu Leu His
10 15 20

aac gtt gcg ggt ttg gac gat tca ctg gcg tgg ttc ttt tcc ctt ttc 211
Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp Phe Phe Ser Leu Phe
25 30 35

ggc ctt gtc atc acg atc cgt gca att atc gcg cct ttc acc tgg cag 259
Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala Pro Phe Thr Trp Gln
40 45 50

atg tat aag tcg ggc cgc act gcc gca cat att cgt cct cac cgc gct 307
Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile Arg Pro His Arg Ala
55 60 65

gcg ctc cgg gaa gaa tac aag gga aag tac gat gaa gcg tcc att cgg 355
Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp Glu Ala Ser Ile Arg
70 75 80 85

gag ttg cag aag cgc cag aat gat ttg aat aag gaa tac ggc att aac 403
Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys Glu Tyr Gly Ile Asn
90 95 100

ccg ctg gca ggt tgt gtg cct ggg ctg atc cag ata ccg att gtc ctt 451
Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln Ile Pro Ile Val Leu
105 110 115

ggc ctt tac tgg gca ctt ctc cgc atg gct cgc cct gaa ggt ggt ttg 499
Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg Pro Glu Gly Gly Leu
120 125 130

gaa aat ccc gtc ttc cag tcg atc ggc ttc cta act cct gag gaa gtg 547
Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu Thr Pro Glu Glu Val
135 140 145

gaa tct ttc ctc gct ggt cgc gtg agc aat gtg cct ctg ccc gct tat 595
Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val Pro Leu Pro Ala Tyr
150 155 160 165

gtt tcg atg ccc act gag cag cta aaa tat ttg agc acc acg cag gcg 643
Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu Ser Thr Thr Gln Ala
170 175 180

gaa gtt ctt agt ttc gtt ttg cca ctg ttc atc aca gcc gca atc ctc 691
Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile Thr Ala Ala Ile Leu
185 190 195

acc gca atc aac atg gcg atg tcc atg tac cgc agc ttc caa acc aac 739
Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg Ser Phe Gln Thr Asn
200 205 210

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gat tac gca tcc gga ttc tct aac ggc atg ctg aag ttc atg atc gtg 787
 Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu Lys Phe Met Ile Val
 215 220 225

atg tcg atc ctc gcg ccg atc ttc cca ctg tcc ctt ggc ctc aca gga 835
 Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser Leu Gly Leu Thr Gly
 230 235 240 245

cca ttc ccc aca gca atc gca ctc tat tgg gtc agc aac aac ctg tgg 883
 Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val Ser Asn Asn Leu Trp
 250 255 260

acg ctc ctc caa aca atc atc atg atg gtc att ttg gaa cgc aaa tac 931
 Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile Leu Glu Arg Lys Tyr
 265 270 275

cca ctt acc gac gat ttc aaa gtg cac cac cta gag cag cgc gac atc 979
 Pro Leu Thr Asp Asp Phe Lys Val His His Leu Glu Gln Arg Asp Ile
 280 285 290

tac cgc gca aaa caa aaa gaa aag cgc atc ttc ctg tgg aca cga cgc 1027
 Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe Leu Trp Thr Arg Arg
 295 300 305

aaa aac cgc gcc ctg atg att ctc acc cca tgg aac gcc tca acg ctt 1075
 Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp Asn Ala Ser Thr Leu
 310 315 320 325

cac gca aca aac gtg gaa ctc acc aaa acc cgt act gcc gaa atc aac 1123
 His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg Thr Ala Glu Ile Asn
 330 335 340

gaa gca aaa cag gcc cgc aaa gaa atc gcg aac aag agg cgc gaa acg 1171
 Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn Lys Arg Arg Glu Thr
 345 350 355

caa cgt gaa atg aac cgc gcc gcc atg cag cgc tta aag cag cgt cgc 1219
 Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg Leu Lys Gln Arg Arg
 360 365 370

gct gag gtt aaa gct aaa aag aag ggg ctt atc gac gcc tcc ccc aac 1267
 Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile Asp Ala Ser Pro Asn
 375 380 385

gaa gat acc cct tcg gaa aat gaa gaa act aaa ttg agt agt ccg cag 1315
 Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys Leu Ser Ser Pro Gln
 390 395 400 405

gtg gag ccg aca aca act gcc gag cca aat cgc gag ccg tct caa gag 1363
 Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg Glu Pro Ser Gln Glu
 410 415 420

gac tgatgttgtg gaccaatcga gat 1389
 Asp

<210> 444

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

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His	Leu	Leu	Leu	His	Asn	Val	Ala	Gly	Leu	Asp	Asp	Ser	Leu	Ala	Trp
			20					25					30		
Phe	Phe	Ser	Leu	Phe	Gly	Leu	Val	Ile	Thr	Ile	Arg	Ala	Ile	Ile	Ala
		35					40					45			
Pro	Phe	Thr	Trp	Gln	Met	Tyr	Lys	Ser	Gly	Arg	Thr	Ala	Ala	His	Ile
	50					55					60				
Arg	Pro	His	Arg	Ala	Ala	Leu	Arg	Glu	Glu	Tyr	Lys	Gly	Lys	Tyr	Asp
65					70					75					80
Glu	Ala	Ser	Ile	Arg	Glu	Leu	Gln	Lys	Arg	Gln	Asn	Asp	Leu	Asn	Lys
				85					90					95	
Glu	Tyr	Gly	Ile	Asn	Pro	Leu	Ala	Gly	Cys	Val	Pro	Gly	Leu	Ile	Gln
			100					105					110		
Ile	Pro	Ile	Val	Leu	Gly	Leu	Tyr	Trp	Ala	Leu	Leu	Arg	Met	Ala	Arg
		115					120						125		
Pro	Glu	Gly	Gly	Leu	Glu	Asn	Pro	Val	Phe	Gln	Ser	Ile	Gly	Phe	Leu
	130					135					140				
Thr	Pro	Glu	Glu	Val	Glu	Ser	Phe	Leu	Ala	Gly	Arg	Val	Ser	Asn	Val
145					150					155					160
Pro	Leu	Pro	Ala	Tyr	Val	Ser	Met	Pro	Thr	Glu	Gln	Leu	Lys	Tyr	Leu
				165					170					175	
Ser	Thr	Thr	Gln	Ala	Glu	Val	Leu	Ser	Phe	Val	Leu	Pro	Leu	Phe	Ile
			180					185					190		
Thr	Ala	Ala	Ile	Leu	Thr	Ala	Ile	Asn	Met	Ala	Met	Ser	Met	Tyr	Arg
		195					200					205			
Ser	Phe	Gln	Thr	Asn	Asp	Tyr	Ala	Ser	Gly	Phe	Ser	Asn	Gly	Met	Leu
	210					215					220				
Lys	Phe	Met	Ile	Val	Met	Ser	Ile	Leu	Ala	Pro	Ile	Phe	Pro	Leu	Ser
225					230					235					240
Leu	Gly	Leu	Thr	Gly	Pro	Phe	Pro	Thr	Ala	Ile	Ala	Leu	Tyr	Trp	Val
				245					250					255	
Ser	Asn	Asn	Leu	Trp	Thr	Leu	Leu	Gln	Thr	Ile	Ile	Met	Met	Val	Ile
			260					265					270		
Leu	Glu	Arg	Lys	Tyr	Pro	Leu	Thr	Asp	Asp	Phe	Lys	Val	His	His	Leu
		275					280					285			
Glu	Gln	Arg	Asp	Ile	Tyr	Arg	Ala	Lys	Gln	Lys	Glu	Lys	Arg	Ile	Phe
	290					295					300				
Leu	Trp	Thr	Arg	Arg	Lys	Asn	Arg	Ala	Leu	Met	Ile	Leu	Thr	Pro	Trp

[illegible]

Parameter	Value	Unit
Initial concentration	100	mg/L
Initial pH	7.0	
Temperature	25	°C
Time	0-120	min
Batch	1	
Batch	2	
Batch	3	
Batch	4	
Batch	5	
Batch	6	
Batch	7	
Batch	8	
Batch	9	
Batch	10	
Batch	11	
Batch	12	
Batch	13	
Batch	14	
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Batch	100	